

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

10

2) INFORMATION FOR SEQ ID NO: 1913

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGGAACC

20

25

2) INFORMATION FOR SEQ ID NO: 1914

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

40 CGCCTTGATC GTTGGGAACC

20

45

2) INFORMATION FOR SEQ ID NO: 1915

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

35 CGTGGGTCTG GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1918

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

50 GTGGGTCTCA CGGTATCATT G

21

2) INFORMATION FOR SEQ ID NO: 1919

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1920

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1921

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

CGTGGGTCTA GCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1922

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTCCAAT GATTAGCACT TTTA

24

10

2) INFORMATION FOR SEQ ID NO: 1923

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTCCAAT GATAAGCACT TTTA

24

25

2) INFORMATION FOR SEQ ID NO: 1924

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

40 GTTTCCAAT GCTGAGCACT TTT

23

2) INFORMATION FOR SEQ ID NO: 1925

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 861 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neisseria meningitidis*
 - 35 (B) STRAIN: MC9690-129
 - (C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40	ATGAGTATTC AACATTTCTG TGTCGCCCTT ATTCCCTTT TTGCGGCATT	50
	TTGCCCTTCCT GTTTTGCTC ACCCAGAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	200
	GAGCACTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGGTGACG	250
45	CCGGGCAAGA GCAAATCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG	450
	CACAAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
50	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAAC GTTGCGCAAA CTATTAAC TG GCGAACTACT TACTCTAGCT	600
	TCCCCGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1928

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: HB251
- (C) ACCESSION NUMBER: X57972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTTC	AACATTTCCG	TGTCGCCCTT	ATTCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTGCTC	ACCCAGAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTCGCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTCTGC	TATGTGGCGC	GGTATTATCC	CGTGGTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTAAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATT	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTG	450
	CACAAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AAACGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAAC	GTTGCGCAAA	CTATTAAC	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GT	TTATTGCT	700
	GAGCCGGTGA	CGGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

2) INFORMATION FOR SEQ ID NO: 1929

- | | | |
|----|-------------------------------|--|
| 50 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 808 bases | |
| | (B) TYPE: Nucleic acid | |
| | (C) STRANDEDNESS: Double | |
| | (D) TOPOLOGY: Linear | |

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: 26W
 (C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

10	ATGAGTATTAC AACATTTCCG TGTCGCCCTT ATTCCCTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCG GAAGAACGTT TTCCAATGAT	200
	GAGCACTTT AAAGTCTGC TATGTGGTGC GGTATTATCC CGTGGTGACG	250
15	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATT A TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG	450
	CACAAACATGG GGGATCATGT AACCCGCCCTT GATAGTTGGG AACCGGAGCT	500
20	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAAC GTTGCACAAA CTATTAACGT GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAAATAGA CTGGATGGAG GCGGATAAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAAATCTG	700
	GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT	750
25	GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC	800
	TATGGATG	808

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

45	ATGAGTATTAC AACATTTCCG TGTCGCCCTT ATTCCCTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCG GAAGAACGTT TTCCAATGAT	200
50	GAGCACTTT AAAGTCTGC TATGTGGCAG GGTATTATCC CGTGGTGACG	250
	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATT A TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400

	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTG	450
	CACAAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCAGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAAC	GTTGCGCAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT	600
5	TCCCCGCAAC	AATTAAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTATTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	GGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
10	AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 1931

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 861 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 20 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 25 (A) ORGANISM: *Escherichia coli*
 - (B) STRAIN: BM2728
 - (C) ACCESSION NUMBER: AF104442
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
35	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATT	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTG	450
40	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCAGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAAC	GTTGCGCAA	CTATTAACTG	GCGAACTACT	TACTCTAGCT	600
	TCCCCGCAAC	AATTAAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTATTATTGCT	GATAAATCTG	700
45	GAGCCGGTGA	GCGTGGGTCT	CTCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190695

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO: 1932

15	ATGAGTATTAC AACATTTCCG TGTCGCCCTT ATTCCCTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT	200
	GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGGTGACG	250
20	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAC GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG	450
	CACAAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
25	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAAC GTTGGCAAA CTATTAACGT GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700
	GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT	750
30	GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC	800
	TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA	850
	AGCATTGGTA A	861

35

2) INFORMATION FOR SEQ_ID NO: 1933

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190693

50 (xi) SEQUENCE DESCRIPTION: SEQ_ID NO: 1933

ATGAGTATTAC AACATTTCCG TGTCGCCCTT ATTCCCTTT TTGCGGCATT	50
TTGCCTTCCT GTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100

	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAGCT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTCGCCCCC	GAAGAACGTT	TTCCAATGGT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGTGC	GGTATTATCC	CGTGGTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
5	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTACGGATG	GCATGACAGT	350
	AAGAGAATT	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTG	450
	CACAACATGG	GGGATCATGT	AACCCGCCTT	GATCGTCGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
10	TGGCAACAAAC	GTTGCGCAAA	CTATTAAC	CGGAAC	TACTCTAGCT	600
	TCCCGGCAAC	AATTAAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GT	TTATTGCT	700
	GAGCCGGTGA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
15	TATGGATGAA	CGAGATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

20 2) INFORMATION FOR SEQ ID NO: 1934

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35 2) INFORMATION FOR SEQ ID NO: 1935

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - 40 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 15 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936

10 TACCA~~CCCGC~~ ACGGC

15

15 2) INFORMATION FOR SEQ ID NO: 1937

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 17 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937

CGGAGTCGCC GTCGATG

17

30 2) INFORMATION FOR SEQ ID NO: 1938

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(i-i) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938

CCGGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G

41

45

2) INFORMATION FOR SEQ ID NO: 1939

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 46 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5

CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCggCC GGGTCG

46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT

19

25.

2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- 30 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT

18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- 45 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

5 2) INFORMATION FOR SEQ ID NO: 1943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20 2) INFORMATION FOR SEQ ID NO: 1944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

2) INFORMATION FOR SEQ ID NO: 1945

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

2) INFORMATION FOR SEQ ID NO: 1946

1013

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

17

- 15 2) INFORMATION FOR SEQ ID NO: 1947

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATAACGG CACCATCGT

19

- 30 2) INFORMATION FOR SEQ ID NO: 1948

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

19

- 45 2) INFORMATION FOR SEQ ID NO: 1949

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 17 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

CCTGCTATGG AGCGATGGT

19

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2) INFORMATION FOR SEQ ID NO: 1953

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

2) INFORMATION FOR SEQ ID NO: 1954

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883
- (C) ACCESSION NUMBER: AF052258

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

ACACCGGTCA	ACATTGAGGA	AGAGCTTAAG	AACTCTTATC	TGGATTATGC	50
GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	GGATGTCCGA	GATGCCCTGA	100
AGCCGGTACA	CCGTCGCGTA	CTTACGCCA	TGAACGTATT	GGGCAATGAC	150
TGGAACAAAG	CCTATAAAAAA	ATCAGCCCGT	GTCGTTGGTG	ACGTAATCGG	200
TAAATACCAAC	CCGCACGGCG	ACTCCGCGGT	ATACGACACC	ATCGTGCCTA	250
TGGCGCAGCC	GTTCTCGCTG	CGTTACATGC	TGGTGGACGG	CCAGGGTAAC	300
15 TTTGGTTCCA	TCGACGGCGA	CTCCGCCCGCG	GCGATGCGTT	ATACCGAAAT	350
TCGTCCTGGCG	AAAATCGCTC	ATGAGCTGAT	GGCCGATCTT	GAAAAAGAGA	400
CGGTCGATTT	CGTCGACAAC	TATGACGGTA	CGGAGCGTAT	TCCGGACGTC	450
ATGCCGACCA	AAATTCTAA	CCTGCTGGTG	AACGGCGCCT	CCGGGATCGC	500
CGTAGGGATG	GCCACCAACA	TACCGCCACA	TAACCTGACG	GAAGTGATTA	550
60 ACGGCTGTCT	GGCGTATGTT	GACGATGAAG	ACATCAGCA		589

2) INFORMATION FOR SEQ ID NO: 1955

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- 15 (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG, TCTGCGCG

38

15

2) INFORMATION FOR SEQ ID NO: 1956

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 989 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida inconspicua*
 - (B) STRAIN: ATCC 16783
- 35 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

CGGTAAAACC	ACTTTAACTG	CTGCAATCAC	CAAAGTTTA	TCTGAAGAAG	50
GTGGTGCAGA	TTTCTTAGAT	TATTCATCTA	TTGATAAAGC	ACCAGAACAGAG	100
35 AGAGCTAGAG	GTATTACCAT	TTCTACTGCT	CATGTTGAAT	ATGAAACTCC	150
AAACAGACAT	TATTACATG	TTGATTGTCC	AGGTCTACAA	GATTATATTA	200
AGAACATGAT	TACTGGTGCA	GCTCAAATGG	ATGGTGCTAT	TATTGTTGTT	250
GCAGCTACTG	ATGGTCAAAT	GCCACAACT	AAGGAACATT	TATTATTAGC	300
TAGACAAGTT	GGTGTCAAC	ATTTAGTTGT	TTTGTTAAC	AAGTGTGATA	350
40 CCGTTGATGA	TCCAGAAATG	TTRGAATTAG	TTGAAATGGA	AATGAGAGAA	400
TTATTGACCG	AATATGGATT	YGATGGTGT	AACACACCAG	TTATTATGGG	450
TTCTGCATTA	ATGGCATTAG	AAGGTAAGAG	ACCAGAACATT	GGTAAAGAAT	500
CTATTGTTAA	GTAAATGGAA	GCTGTTGATA	CTTGGATTCC	AACTCCACAA	550
45 AGAGACTTAG	AAAAACCATT	CTTATTACCA	ATTGATGAAG	TTTTCTCTAT	600
TTCTGGTAGA	GGTACTGTTG	TTTCTGGTAC	TGTTGATAGA	GGTACATTAA	650
AGAAGGGTGA	AGAAGTTGAA	ATTGTTGGTG	GTAAAGAACAG	TGTTATTAAG	700
ACTACTGTTA	CCGGTATTGA	AATGTATCAC	AAGGAATTAG	ATCAAGCACA	750
AGCTGGTGAT	ACTCCAGGTA	TTTGTTAACG	AGGTGTTAACG	AGAGATCAA	800
TTGCAAGAGG	TCAAATTCTT	GCAAAGCCAG	GWTCTGTTAA	GGCATACAAAG	850
50 AAGTTCTTAT	CATCATTATA	CATTTAACAA	AAGGAAGAACG	GTGGTAGACA	900
TACTCCATT	TCTGAAAATT	ACAGACCTCA	AATGTACATT	AGAACTTCCA	950
ATGTTAATGT	TACTTGAAG	TTCCCAGAAA	CTGAAGAACG		989

2) INFORMATION FOR SEQ ID NO: 1957

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
- (B) STRAIN: ATCC 22023

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

GGTAAGACCA	CCCTTACTGC	CGCCATCAC	AAGTGCCTTG	CTGAGAAGGG	50
AGGTGCCTCG	TTCTTGGACT	ACAGTGCCAT	CGACAAGGCG	CCAGAGGAGA	100
GAGCAAGAGG	TATCACCATC	TCCACTGCGC	ACGTTGAGTA	TGAAACTGCC	150
20 AACAGACACT	ACTCGCACGT	TGACTGTCCA	GGTCACGCTG	ATTACATCAA	200
GAACATGATT	ACCGGTGCTG	CGCAGATGGA	CGGTGCTATC	ATTGTCGTTG	250
CAGCCACTGA	CGGTCAAGATG	CCACAGACCA	GAGAACACTT	GTTGCTTGCC	300
AGACAAGTTG	GTGTCCAGCA	CATTGTTGTC	TTCGTCAACA	AGGTTGACAC	350
25 CATCGACGAC	CCTGAGATGC	TTGAGCTTGT	TGAAATGGAG	ATGAGAGAGT	400
TGCTTACTTC	GTATGGATT	GACGGTGATA	ACACCCCAGT	TATCATGGGT	450
TCTGCTTTGT	GTGCTTGGA	AGGCCGTGAG	CCAGAGATTG	GTGCTAAGGC	500
CATTGACAAG	TTGATGGAGG	CCATTGATGA	GTACATCCC	ACTCCTCAGA	550
GAGACCTGGA	AAAGCCATT	YTGATGGGTG	TTGAAGACGT	GTTCTCGATC	600
30 TCTGGTAGAG	GTACCGTTGT	CACRGCCGT	GTTGAGCGTG	GTAACATTGAA	650
GAAAGGTGAT	GAAATTGAAC	TTGTTGGCTA	CAACAAGAAC	CCAATCAAGA	700
CCACCGTCAC	CGGTATCGAA	ATGTTCAAGA	AGGAGTTGGA	ATCTGCCATG	750
GCTGGTGACA	ACTGTGGTAT	CTTGTGCGT	GGTATCAAGA	GAGATGACGT	800
CAAGAGAGGT	ATGGTTGCTG	CTAACGCCAGG	CTCCGTCTCT	GCACACACCA	850
35 AGTCCTCGC	TTCCTGTAC	ATCCTGACRA	AGGAGGAAGG	TGGTCGTCAC	900
AGTGCCTTG	CTGAGAACTA	CAGACCACAG	ATGTTCATCA	GAACCGGAGA	950
TGTCACCACC	ATCTTGACAT	GGCCAGAGGA	GCACGCTGAC	C	991

40 2) INFORMATION FOR SEQ ID NO: 1958

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
- (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC ACTTTGACCG CCGCCATCAC CAAGGTGTTG AGGCCAAAG	50
	GTGGTGCTTC CTTCTGGAC TACGGTCCA TCGACAGAGC CCCTGAGGAG	100
5	AGAGCCAGAG GTATTACTAT CTCGACTGCC CACGTTGAGT ACGAGACCGA	150
	TAAGAGACAC TACGCCACG TTGATTGCC TGTCACGCT GATTACATCA	200
	AGAACATGAT CACTGGTGC GCCCAAATGG ACGGTGCCAT TATTGTCGTT	250
	GCTGCTCTG ATGGCAAAT GCCGAGACC AGAGAGCACT TGTTGCTTGC	300
	CAGACAGGTT GGTGTGCAGA ACTTGGTTGT GTTGTTAAC AAGGTGGACA	350
10	CCATCGACGA CCCCAGAAATG TTGGAGTTGG TGAGATGGA AATGAGAGAA	400
	TTGTTGACCC ACTACGGCTT TGACGGTGAC AACACCCCTG TCATCATGGG	450
	TTCGGCGTTG TGTGCCTTGG AAGACAGGCA GCCTGAGATT GGCGAGCAAG	500
	CCATCATGAA GTTGTGGAC GCTGTCGACG AGTACATTCC CACTCCTCAG	550
	AGAGACTTGG AGCAACCATT TTTGATGCCG GTTGAGGATG TTTTCTCCAT	600
15	CTCTGGCAGA GGTACTGTTG TCACCGGTG TGTTGAGAGA GGCTCATTGA	650
	AGAAGGGTGA GGAGATTGAG ATTGTTGGCG ACTTCCCCAA GCCCTTCAAG	700
	ACTACCGTCA CGGGCATTGA GATGTTCAAG AAGGAGTTGG ATGCCCGCAT	750
	GGCGGGCGAC AACGCCGGGA TCTTGTGAG AGGTGTCAAG AGAGACGAGG	800
	TCTCGAGAGG TATGGTTTG GCCAAGCCCCG GTACTGTCAC TTGCGCACACC	850
20	AAGGTGTTGG CGTCGCTTTA CATCTTGACC AAAGAGGAAG GTGGCCGCCA	900
	CTCGCCCTTT GGTGAGAACT ACAAGCCACA GTTATTCATC AGAACCTCCG	950
	ATGTCACTGG TACTTGAGG TTCCCCGCCG GTGAG	985

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
- (B) STRAIN: ATCC 10565
- (C) ACCESSION NUMBER:

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC ACCTTGACTG CCGCCATCAC CAAGGTCTC TCCGAGAAGG	50
	GTGGTGCCGA CTTCTGGAC TACGGTGCCA TTGACAGAGC CCCCCGAGGAG	100
15	CGTCCCCGTG GTATCACCAT CTCCACTGCC CACGTTGAGT ACGAGACTGA	150
	CAACCGTCAC TACGCCACA TTGACTGTCC CGGTACGCT GATTACATCA	200
	AGAACATGAT TACCGGTGCC GCCCAGATGG ACGGTGCCAT TATTGTCCTT	250
	GCTGCTACTG ACGGTGCCAT GCCCCAGACC CGCGAGCACT TGTTCTCGC	300
	CCGTCAAGGTT GGTATCCAGG AATTGGTTGT GTTGTTAAC AAGGTTGACA	350
50	CCATCGACGA CCCCAGATG TTGGAGCTCG TTGAGATGGA GATCCCGCAG	400
	TTGTTGCTG AGTTGGTT TGACGGTGAC AACACCCCCG TCATCATGGG	450
	TTCCGCTTTG TGCGCTTGG AGGGCAAGCA GCCCGAGATT GGTGAGCAGG	500
	CTATCACCAA GTTGATGGCC GCCGTTGACG AGCACATCCC CACCCCCCAG	550

	CGTGACTTGG AGCAGCCCTT CTTGATGCCCT GTTGAGGGTG TTTTCTCTAT	600
	CTCTGGCCGT GGTACCGTGG TGACTGGTAA GGGTGCCTCGT GGTGTCCTCA	650
	AGAAGGGTGA GGAGATTGAG ATTGTTGGCA ACTTTGACAA GCCCTACAAG	700
5	GTGACTGTTA CTGGTATTGA GATGTTCAAG AAGGAGTTGG ACCAGGCCAT	750
	GGCTGGTGAC AACGCCGGTA TCTTGTGCG TGGTGTCAAG CGTGACGAGG	800
	TGTCTCGTGG TATGGTTTG GCCAAGCCCC GCACTGTTGT CTCGCCACAAG	850
	AAGGTTTGG CTTCGCTTTA CATCTTGACC CAGGAGGAGG GTGGCCGTAA	900
	GACCGGCTTC GGCTCCAAC ACAAGCCCCA GTTGTCTTG CGCACTACCG	950
	ACGTCACTGG TACCCCTCACCC TTC	973

10

2) INFORMATION FOR SEQ ID NO: 1960

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
- (B) STRAIN: ATCC 28870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

	AAGACTACCT TGACTGCTGC AATCACCAAG GTCTTAGCTG ATCAAGGTGG	50
30	TGCTGATTTC TTAGATTATG CATCTATTGA CAAGGCTCCT GAAGAAAGAG	100
	CAAGAGGTAT TACTATCTCT ACTGCTCACG TTGAGTATGA AACCCCAAAC	150
	AGACATTATT CTCATGTCGA TTGTCCTGGC CATCAAGATT ATATAAGAA	200
	TATGATTACT GGTGCTGCAC AAATGGATGG TGCTATTATT GTTGTGCTG	250
35	CTACTGATGG TCAAATGCCA CAAACTAAGG AACATTTATT ATTAGCAAGA	300
	CAAGTTGGTG TTCAACATT AGTTGTCTT GTTAATAAAAT GTGACACCAT	350
	TGATGACCCA GAAATGTTGG AATTAGTGA AATGGAAATG AGAGAACTAT	400
	TGTCTGAATA TGGTTTGAT GGTGATAACA CTCCAGTTAT TATGGGTTCT	450
	GCATTGATGG CTTTAGAAGA CAAGAGACCT GAAGTTGGTA AGGAATCTAT	500
	TTTAAAGTTA ATGGAAGCYG TTGACACATG GATTCCAACC CCAGAGAGAG	550
40	ATTTAGAAAA ACCATTTTG TTACCTATTG ATGAAGTTT CTCAATCTCT	600
	GGTAGAGGTA CTGTCGTTTC TGGTACTGTC GAAAGAGGTA CTTTGAAGAA	650
	GGGTGAAGAA GTTGAAATTG TTGGTGGTAA GGATGGTTCT ATTAAAACCA	700
	CTGTCACAGG TATTGAAATG TATCACAAGG AATTAGACCA AGCGCAAGCA	750
45	GGTGATACTC CAGGTATTTT ATTAAGAGGT GTCAAGAGAG ACCAAATCAA	800
	GAGAGGTCAA ATTTTAGCAA AGCCAGATTC CGTTAAGGCA TACAAGAAGT	850
	TCTTGGCTTC CCTTTATATC TTAACCAAGG AAGAAGGTGG TAGACATACA	900
	CCATTCTCTG AAAACTACAG ACCACAAATG TACATCAGAA CTACCAATGT	950
	TAACGTTACT TTGAAGTTCC CAGACACTGA AGAAG	985

50

2) INFORMATION FOR SEQ ID NO: 1961

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961
10 GCTCAAGGCA GATGGCATTC CC 22

15 2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962
25 GGACAAGGCG GTTGCCTTG AT 22

30 2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963
CATTCCCGTC TCGCTCGACA GT 22

45 2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5

ATCTGCCTGC CCGTCTTGC

19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05
- (C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25	ATGAATAAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG	50
	TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG	100
	CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CGGTCCGGCA	150
	TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG	200
30	TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGCTCTCGC	250
	TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTG GC GTGGTGTG	300
	GCCTATCTCA ATGATATTG CGGTTTCCA GACGCTGCGT TCTATCCGCA	350
	ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTG GTGCAAGACG	400
	GGCAGGCAGA TCGGCCGAG GCACCCGCTG GCGACATCAT GGATCACATT	450
35	GCGGCGTTCT TTGACCGCGC CATCGCGCG CTGACGGGTG CCGGTATCAA	500
	ACGCAACCGC CTTGTCCTTG ATCCC GGCCAT GGGGTTTTT CTGGGGCTG	550
	CTCCC GAAAC CTCGCTCTCG GTGCTGGCGC GGTTCGATGA ATTGCGGCTG	600
	CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTCTGCG	650
	CGCGCTCAC A GGCGTGGTC CGGGGGATGT CGGGGCCGCG ACACTCGCTG	700
40	CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG	750
	CCCGCGCCCT TGCGCGACGG GCTGGCGTA TTGGCGCGC TGAAAGAAC	800
	CGCAAGAATT CGTTAA	816

15

2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 50 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG

19

2) INFORMATION FOR SEQ ID NO: 1967

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20 CAGCAATAAG TAATCCAGCG ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1968

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATT CACCGCATAG

20

40 2) INFORMATION FOR SEQ ID NO: 1969

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1970

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1206 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Transposon Tn10
 (C) ACCESSION NUMBER: J01830

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

ATGAATAGTT	CGACAAAGAT	CGCATTGGTA	ATTACGTTAC	TCGATGCCAT	50
GGGGATTGGC	CTTATCATGC	CAGTCTGCC	AACGTTATTA	CGTGAATTAA	100
TTGCTTCGGA	AGATATCGCT	AACCACTTG	GCGTATTGCT	TGCACCTTAT	150
20 GCGTTAACATGC	AGGTTATCTT	TGCTCCTGG	CTTGGAAAAA	TGTCTGACCG	200
ATTGGTCGG	CGCCCGATGC	TGTTGTTGTC	ATTAATAGGC	GCATCGCTGG	250
ATTACTTATT	GCTGGCTTT	TCAAGTGCAC	TTTGGATGCT	GTATTAGGC	300
CGTTGCTTT	CAGGGATCAC	AGGAGCTACT	GGGGCTGTCG	CGGCATCGGT	350
CATTGCCGAT	ACCACCTCAG	CTTCTCAACG	CGTGAAGTGG	TTCGGTTGGT	400
25 TAGGGGCAAG	TTTTGGGCTT	GGTTAACAG	CGGGGCCTAT	TATTGGTGGT	450
TTTGCAGGAG	AGATTCACC	GCATAGTCCC	TTTTTATCG	CTGCCTTGCT	500
AAATATTGTC	ACTTCCCTG	TGGTTATGTT	TTGGTTCCGT	GAAACCAAAA	550
ATACACGTGA	TAATACAGAT	ACCGAAGTAG	GGGTTGAGAC	GCAATCGAAT	600
TCGGTATAACA	TCACTTTATT	TAAAACGATG	CCCATTGTTG	TGATTATTAA	650
30 TTTTCAGCG	CAATTGATAG	GCCAAATTCC	CGCAACGGTG	TGGGTGCTAT	700
TTACCGAAAA	TCGTTTGGG	TGGAATAGCA	TGATGGTTGG	CTTTTCATTA	750
GCGGGTCTTG	GTCTTTACA	CTCAGTATTG	CAAGCCTTG	TGGCAGGAAG	800
AATAGCCACT	AAATGGGGCG	AAAAAACGGC	AGTACTGCTC	GAATTATTG	850
CAGATAGTAG	TGCATTGCC	TTTTAGCGT	TTATATCTGA	AGGTTGGTTA	900
35 GATTCCCTG	TTTAATTTT	ATTGGCTGGT	GGTGGGATCG	CTTTACCTGC	950
ATTACAGGGA	GTGATGTCTA	TCCAAACAAA	GAGTCATGAG	CAAGGTGCTT	1000
TACAGGGATT	ATTGGTGAGC	CTTACCAATG	CAACCGGTGT	TATTGGCCCA	1050
TTACTGTTA	CTGTTATTAA	TAATCATTCA	CTACCAATTG	GGGATGGCTG	1100
GATTGGATT	ATTGGTTAG	CGTTTACTG	TATTATTATC	CTGCTATCGA	1150
40 TGACCTTCAT	GTAAACCCCT	CAAGCTCAGG	GGAGTAAACA	GGAGACAAGT	1200
GCTTAG					1206

45 2) INFORMATION FOR SEQ ID NO: 1971

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

CYGACTGYGC CATCCTYATC A

21

5

2) INFORMATION FOR SEQ ID NO: 1972

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

MGICAGCTCA TYITTGCWKS C

21

20

2) INFORMATION FOR SEQ ID NO: 1973

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50 ACAAGGGITG GRMSAAGGAG AC

22

2) INFORMATION FOR SEQ ID NO: 1975

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTTRAGGAC G

21

2) INFORMATION FOR SEQ ID NO: 1976

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

2) INFORMATION FOR SEQ ID NO: 1977

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

45 GATGGAYTCY GTYAARTGGG A

21

2) INFORMATION FOR SEQ ID NO: 1978

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

10 CATCITGYAA TGGYAATCTY AAT

23

10 2) INFORMATION FOR SEQ ID NO: 1979

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

25 CATCYTGYAA TGGYAASCTY AAT

23

2) INFORMATION FOR SEQ ID NO: 1980

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40 TCRATGGCIT CIAIRAGRGT YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCAC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50 CYGAYTGYGC YATYCTSATC A

21

2) INFORMATION FOR SEQ ID NO: 1985

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: M1-106
 (C) ACCESSION NUMBER: U81804

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20 TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
AAGTCTTCTT	TCAAGTACGC	TTGGGTTCTT	GACAAGCTTA	AGGCCGAGCG	200
AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
AGTACCAAGT	TACCGTCATT	GACGCCCG	GTCACCGAGA	CTTCATCAAG	300
AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTGC	350
25 CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
GAGAGCACCG	CCTCCCGGCC	TTCACCCCTCG	GTGTCAGGCA	GCTCATTGTT	450
GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
AATCGTCAAG	GAGACCAACG	GTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30 GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
GTCCGGTGT	TCCAAGGGTA	AGACCCTCT	CGAGGCCATC	GACGCCAGTA	700
GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTCGCCCCC	ACCAACGTCA	850
35 CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
ATCGGTGCCG	GTTACACCCC	CGTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40 TTGCAAGTTC	TCTGAGTTGA	TCGAGAAAGAT	TGACCGACGA	ACCGGTAAGG	1150
TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
AAGCTTGT	CCCAGAAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
CCCTCTTGGT	CGATTGCCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
45 AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

2) INFORMATION FOR SEQ ID NO: 1986

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: B3501
- (C) ACCESSION NUMBER: U81803

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15 TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
AAGTCTTCTT	TCAAGTACGC	TTGGGTTCTT	GACAAGCTTA	AGGCCGAGCG	200
AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
GGTACCAAGGT	CACCGTCATT	GACGCCCG	GTCACCGAGA	CTTCATCAAG	300
AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTTGC	350
20 CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
GAGAGCACGC	CCTCCTCGCC	TTCACCCCTCG	GTGTCAGGCA	GCTCATTGTT	450
GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
AATCGTCAAG	GAGACCAACG	GTTCATCAA	GAAGGTTGGC	TACAACCCCCA	550
AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25 GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
GTCTGGTGT	TCCAGGGTA	AGACCCTCT	CGAGGCCATC	AGCCGCCAGTA	700
GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
CGGTGTACATC	AAGGCCGGTA	TGGTCGTCAA	GTTGCCCCCC	ACCAACGTCA	850
30 CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTT	CCATCAAGGA	950
CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35 CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
AAGCTTGTG	CCCAGAAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
CCCTCTTGGT	CGATTCGCCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGCAA	GGTCACCAAG	1350
40 GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: X01638

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

	ATGGGTAAAG AGAAGTCTCA CATTaacgtt GTCGTTATCG GTCATGTCGA	50
	TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTACAAG TGTGGTGGTA	100
	TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT	150
10	AAGGGTTCTT TCAAGTACGC TTGGGTTTG GACAAGTTAA AGGCTGAAAG	200
	AGAAAAGAGGT ATCACTATCG ATATTGCTT GTGGAAGTTC GAAACTCCAA	250
	AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG	300
	AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC	350
	TGGTGGTGTC GGTGAATTGAG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA	400
15	GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT	450
	GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA	500
	AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA	550
	AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT	600
	GAAGCTACCA CCAACGCTCC ATGGTACAAG GTTGGGAAA AGGAAACCAA	650
20	GGCCGGTGTGTC GTCAAGGGTA AGACTTGTGTT GGAAGCCATT GACGCCATTG	700
	AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT	750
	GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTGAAAC	800
	CGGTGTCATC AAGCCAGGTA TGGTTGTAC TTTCGCCCCA GCTGGTGTAA	850
	CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAAATT GGAACAAGGT	900
25	GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA	950
	AATCAGAAGA GGTAAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG	1000
	GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA	1050
	ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC	1100
	TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA	1150
30	AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTGGTC	1200
	AAGTTCGTTC CATCTAAGCC AATGTGTGTT GAAAGCTTCA GTGAATAACCC	1250
	ACCATTAGGT AGATTGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG	1300
	GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG	1350
	GCTGCTCAAA AGGCTGCTAA GAAATAA	1377

35

2) INFORMATION FOR SEQ ID NO: 1988

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: M10992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

	ATGGGTAAAG AGAAGTCTCA CATTAAACGTT GTCGTTATCG GTCATGTCGA	50
	TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTACAAG TGTGGTGGTA	100
	TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT	150
5	AAGGGTTCTT TCAAGTACGC TTGGGTTTG GACAAGTTAA AGGCTGAAAG	200
	AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA	250
	AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG	300
	AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC	350
	TGGTGGTGTC GGTGAATTGCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA	400
	GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT	450
10	GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA	500
	AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA	550
	AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT	600
	GAAGCTACCA CCAACGCTCC ATGGTACAAG GTTGGGAAA AGGAAACCAA	650
	GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGGCCATT GACGCCATTG	700
15	AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT	750
	GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC	800
	CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTCCCCCA GCTGGTGTAA	850
	CCACTGAAGT CAAGTCCGTT GAAATGCATC ACAGAACAAATT GGAACAAGGT	900
	GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTT CCGTTAAGGA	950
20	AATCAGAAGA GGTAAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG	1000
	GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTGAACCA TCCAGGTCAA	1050
	ATCTCTGCTG GTTACTCTCC AGTTTGAT TGTCACACTG CTCACATTGC	1100
	TTGTAGATTG GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA	1150
	AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTGGTC	1200
25	AAGTCGTT CATCTAACGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC	1250
	ACCATTAGGT AGATTGCGTG TCAGAGACAT GAGACAAACT GTCGCTGTCG	1300
	GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG	1350
	GCTGCTAAA AGGCTGCTAA GAAATAA	1377

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2) INFORMATION FOR SEQ ID NO: 1989

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1377 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 40 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Eremothecium gossypii*
 - (B) STRAIN: ATCC 10895
 - (C) ACCESSION NUMBER: X73978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

50	ATGGGTAAAG AAAAGACTCA CGTTAACGTT GTCGTCATCG GTCACGTCGA	50
	CTCTGGTAAG TCTACTACCA CCGGTCACTT GATCTACAAG TGTGGTGGTA	100
	TTGACAAGAG AACCATCGAG AAGTTCGAGA AGGAGGCTGC CGAGTTGGGT	150
	AAGGGTTCTT TCAAGTACGC CTGGGTTTG GACAAATTGA AGGCTGAGAG	200
	AGAGAGAGGT ATCACCATCG ACATTGCGTT GTGGAAGTTC GAGACTCCAA	250

	AGTACCACGT	CACTGTCATT	GACGCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
	TGGTGGTGT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
5	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550
	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGT	GTCAAGGGTA	AGACCTTGT	GGAGGCCATT	GACGCCATTG	700
10	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTCAACGTC	AGAACGTCT	CCGTCAAGGA	950
15	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
20	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
	ACCATTGGGT	AGATTGCGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTGCG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCAAA	AGGCTGGTAA	GAAATAG			1377

25

2) INFORMATION FOR SEQ ID NO: 1990

	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 1377 bases	
	(B) TYPE: Nucleic acid	
	(C) STRANDEDNESS: Double	
	(D) TOPOLOGY: Linear	
35	(ii) MOLECULE TYPE: Genomic DNA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: <i>Eremothecium gossypii</i>	
	(C) ACCESSION NUMBER: A29820	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990	
	ATGGGTAAGG AAAAGACTCA CGTTAACGTT GTCGTCATCG GTCACGTCGA	50
	CTCTGGTAAG TCTACTACCA CCGGTCACCT GATCTACAAG TGTGGTGGTA	100
45	TTGACAAGAG AACCATCGAG AAGTTCGAGA AGGAGGCTGC CGAGGTTGGGT	150
	AAGGGTTCTT TCAAGTACGC CTGGGTTTTG GACAAATTGA AGGCTGAGAG	200
	AGAGAGAGGT ATCACCATCG ACATTGCGTT GTGGAAGTTC GAGACTCCAA	250
	AGTACCACGT CACTGTCATT GACCCCCCAG GCCACAGAGA CTTCATCAAG	300
	AACATGATTA CCGGTACTTC TCAAGCTGAC TGTGCCATCT TGATCATTGC	350
50	TGGTGGTGTGTC GGTGAGTTCG AGGCTGGTAT CTCCAAGGAC GGTCAGACCA	400
	GAGAGCACGC TTTGTGGCT TACACCTTGG GTGTCAAGCA GTTGATCGTT	450
	GCCATCAACA AGATGGACTC CGTCAAGTGG GACGAGTCCA GATACCAGGA	500
	GATTGTCAAG GAGACCTCCA ACTTCATCAA GAAGGTCGGT TACAACCCTA	550

	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCAAAG	TTCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATTGGGT	AGATTGCGCTG	TCAGAGACAT	GAGACAGACCC	GTTGCTGTCG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCAAA	AGGCTGGTAA	GAAATAG			1377

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2) INFORMATION FOR SEQ ID NO: 1991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*
- (B) STRAIN: KBN616
- (C) ACCESSION NUMBER: AB007770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTCGTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGTTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCTCCG	GTACTGGTGA	500
	ATTCGAGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTCAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTTC	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCCCTTCG	700
	TCCCCATCTC	CGGTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCTGTT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCGT	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
5	TGGTATGGTC	GTTACTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
	CGGTTGAAAT	GCACCACCAAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCCTCA	1150
	ACGCCCAGGT	CATCGCCTT	AACCACCCCG	GTCAGGTCGG	CAACGGTTAC	1200
10	GCTCCCGTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTCGCTGA	1250
	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCCTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTC	1450
15	ACATATTTTC	ACGCCTCGTC	CCACTCTTT	TCCTCCCTTC	CTCTTTGGTT	1500
	CCCCTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAACGTGTTG	CCGTCGGAGT	TATCAAGTCG	GTGAGAAGA	ACACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCCCAGAA	GGCTGGCAAG	AAATAA	1646

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2) INFORMATION FOR SEQ ID NO: 1992

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1380 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Aureobasidium pullulans*
 - (B) STRAIN: R106
 - (C) ACCESSION NUMBER: U19723

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTCCCT	TCAAGTACGC	CTGGGTCCCTC	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCGCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTTC	TCATCATTC	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACCG	CCTTCTCGCC	TACACCCCTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCC	GTTACCAAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTCATCAA	GAAGGTGGC	TACAACCCCCA	550
	AGCACGTTCC	CTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAACTGCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTGGTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCCTCC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

	TACCATCAAG	GGTGGTATGG	TCGTCACCTT	CGCCCCCGCT	GGTGTACCA	850
	CTGAGGTCAA	GTCCGTCGAG	ATGCACCACG	AGCAGCTCTC	CGAGGGTCTC	900
	CCCGGTGACA	ACGTCGGCTT	CAACGTCAAG	AACGTCTCCG	TCAAGGAGAT	950
	CCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTT	1000
5	GCGACTCCTT	CAACGCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAAGGTC	1050
	GGTGCTGGTT	ACGCACCCGT	CCTCGATTGC	CACACTGCC	ACATCGCCTG	1100
	CAAGTTCTCC	GAGCTTGTG	AGAAGATTGA	CCGCCGTACC	GGCAAGTCCG	1150
	TTGAGGCCGC	CCCCAAGTTC	ATCAAGTCTG	GTGACGCCGC	CATCGTCAAG	1200
	ATGGTTCCCT	CCAAGCCTAT	GTGTGTTGAG	GCTTCACTG	ACTACCCTCC	1250
10	TCTCGGTCTG	TTCGCCGTCC	GTGACATGAG	ACAGACCGTC	GCTGTCGGTG	1300
	TCATCAAGTC	CGTCGCCAAG	TCCGACAAGC	AGGGTGCCGG	TAAGGTTACC	1350
	AAGGCCGCTG	TCAAGGCTGG	CAAGAAGTAA			1380

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2) INFORMATION FOR SEQ ID NO: 1993

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1383 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Histoplasma capsulatum*
 - (B) STRAIN: 186AS
 - (C) ACCESSION NUMBER: U14100

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

	ATGGGTAAGG	AAGACAAGAC	TCACATTAAC	CTCGTCGTCA	TCGGCCACGT	50
	CGATTGGGGC	AAATCTACCA	CCACTGGTCA	TTTGATCTAC	AAATGCGGTG	100
35	GTATTGACAG	CCGTACCAATT	GAGAAGTTCG	AAAAGGAAGC	CGAACAGAGTTG	150
	GGCAAGAAAT	CCTTCAAATA	TGCGTGGGTC	CTTGACAAAC	TGAAGTCTGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATTGC	CCTCTGGAAA	TTCGAGACTC	250
	CGAAGTACAG	TGTCACTGTC	ATTGATGCTC	CCGGCCATCG	TGACTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GACTGCGCTA	TCCTCATCAT	350
40	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
	CTCGTGAGCA	CGCTCTGCTT	GCTTTCACCC	TTGGTGTGAG	GCAACTCATC	450
	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTCAA	500
	CGAAATCATC	AAGGAGGTTT	CCAACTTCAT	CAAGAAGGTC	GGATATAACC	550
	CCAAGGCTGT	TCCCCTCGTG	CCAATCTCTG	GTTCGAGGG	TGACAACATG	600
45	ATTGAACCCCT	CCCCCAACTG	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	650
	TGCCTCTGGC	AAGTCTTCTG	GTAAAACCCCT	TCTCGATGCC	ATTGACGCCA	700
	TTGAACCCCC	AACCCGTCTT	ACCGATAAGC	CCCTCCGTCT	TCCCCCTCCAG	750
	GATGTGTACA	AAATCTCTGG	TATTGGCACT	GTTCGGTCTG	GACGTGTTGA	800
	GACTGGTGTG	ATCAAGCCCG	GTATGGTCGT	GACTTCGCT	CCCTCCAACG	850
50	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	ACCAACCAACA	ACTCCAGGCT	900
	GGTTACCCCTG	GCGACAAACGT	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	950
	GGAAGTCCGC	CGTGGCAACG	TTGCTGGCGA	CTCCAAAAAT	GATCCCCCTA	1000
	AGGGCTGCGA	ATCCTTCAAT	GCCCAGGTCA	TCGTCCTTAA	CCACCCCGGC	1050

CAGGGTTGGCG	CTGGTTATGC	CCCAGTCCTC	GACTGCCACA	CTGCCACAT	1100	
TGCTTGCAGG	TTCTCTGAGC	TTATTGAGAA	GATCGACCAGC	CGTACCGGAA	1150	
AGTCTGTTGA	GAACAAACCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCTATC	1200	
GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTGGAGCCCT	TCACTGACTA	1250	
5	TCCCCCTCTT	GGACGTTTCG	CTGTCCGTGA	CATGAGACAA	ACCGTCGCTG	1300
TCGGTGTCAT	CAAGTCCGTC	ATCAAGTCTG	ACAAGACTGC	TGGCAAGGTC	1350	
ACCAAGGCCG	CGCAGAAGGC	CACCAAGAAA	TAA		1383	

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2) INFORMATION FOR SEQ ID NO: 1994

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1383 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- 20 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neurospora crassa*
 - (C) ACCESSION NUMBER: D45837

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

ATGGGCAAGG	AGGACAAGAC	TCACATCAAC	GTCGTCGTTA	TCGGCCACGT	50	
CGATTCCGGC	AAGTCTACCA	CTACCGGTCA	CTTGATCTAC	AAGTGCAGGTG	100	
GTATCGACAA	GCGTACCATC	GAGAAGTTCG	AGAAGGAAGC	CGCTGAGCTC	150	
30	GGTAAGGGTT	CCTTCAAGTA	TGCGCTGGTT	CTTGACAAGC	TCAGGCCGA	200
GCCTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	TTCGAGACTC	250	
CCAAGTACTA	CGTCACCGTC	ATCGATGCC	CCGGTCATCG	TGATTCATC	300	
AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GATTGCGCTA	TCCTCATCAT	350	
TGCCGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGCCAGA	400	
35	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GCAGCTCATT	450
GTTGCCATCA	ACAAGATGGA	CACCACCCAG	TGGTCCCAGA	CTCGTTTCGA	500	
GGAGATCATC	AAGGAGACCA	AGAACCTTCAT	CAAGAAGGTT	GGCTACAACC	550	
CCGCTGGTGT	CGCTTCGTC	CCCATCTCCG	GCTTCAACGG	CGACAAACATG	600	
CTTGAGCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	650	
40	CAAGGCCGGC	AAGGCCACTG	GCAAGACCT	CCTCGAGGCC	ATCGACGCCA	700
TTGAGCCCCC	CAAGCGTCCT	ACCGACAAGC	CCCTCCGTCT	TCCCCCTCCAG	750	
GATGTCTACA	AGATCGGTGG	TATCGGCACA	GTGCCCGTCG	GGCGTATCGA	800	
GACTGGTGTC	CTCAAGCCCC	GTATGGTCGT	TACCTTCGCT	CCTTCCAACG	850	
TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTTGCTCAG	900	
45	GGTGTCCCCG	GTGACAACGT	CGGCTTCAAC	GTGAAGAACG	TTTCCGTCAA	950
GGATATCCGC	CGTGGTAACG	TTGCCGGTGA	CTCCAAGAAC	GACCCCCCTG	1000	
CTGGCGCCGC	CTCTTCACC	GCCCAGGTCA	TCGTTCTCAA	CCACCCCGGT	1050	
CAGGTCGGTG	CCCGCTACGC	CCCCGTCTC	GACTGCCACA	CTGCCACAT	1100	
TGCCCTGCAAG	TTCGCCGAGC	TCCTCGAGAA	GATCGACCAGC	CGTACTGGTA	1150	
50	AGGCTGTTGA	GGCCTCCCCC	AAGTTCATCA	AGTCTGGTGA	TGCTGCCATC	1200
GTCAAGATGA	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACCGACTA	1250	
CCCTCCCCCTC	GGCCGTTTCG	CCGTCGTCGA	CATGCGTCAG	ACCGTCGCG	1300	
TCGGTGTCAT	CAAGGCCGTC	GACAAGTCCA	CCGCTGCCGC	TGGCAAGGTC	1350	

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

5 2) INFORMATION FOR SEQ ID NO: 1995

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 10 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospora anserina*
 (C) ACCESSION NUMBER: X74799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20	ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT	50
	CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCAGTG	100
	GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC	150
	GGCAAGGGCT CTTTCAAGTA TGCCTGGTGT CTTGACAAGT TGAAGGCCGA	200
25	GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTGAGACCC	250
	CCAAGTACTA TGTCACCGTC ATTGATGCC CCGGCCATCG TGATTTCATC	300
	AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT	350
	TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA	400
	CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC	450
30	GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGTTCAA	500
	CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC	550
	CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTCAACGG CGACAACATG	600
	CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT	650
	CAAGGGTGGC AAGGCCACCG GCAAGACCT CTTGAGGCC ATCGACTCCA	700
35	TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG	750
	GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA	800
	GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG	850
	TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG	900
	GGTGTCCCCG GTGACAACGT TGGTTCAAC GTGAAGAACG TCTCCGTCAA	950
40	GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCC	1000
	TGGCGCCGC CTCTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC	1050
	CAGGTCGGTG CTGGTTACGC CCCCGTCCTC GATTGCCACA CTGCCACAT	1100
	CGCTCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA	1150
	AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC	1200
45	GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA	1250
	CCCTCCCCCTC GGTGCTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG	1300
	TCGGTGTCAAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT	1350
	ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA	1383

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2) INFORMATION FOR SEQ ID NO: 1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Podospora curvicolla*
- (B) STRAIN: VLV
- (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

15	ATGGGCAAGG	AGGACAAGAC	TCACATCAAC	GTCGTCGTTA	TCGGCCACGT	50
	CGATTCCGGC	AAGTCGACCA	CCACTGGTCA	CTTGATCTAC	AAGTGCAGGTG	100
	GTATTGACAA	GCGTACCATC	GAGAAGTTG	AGAAGGAAGC	TGCTGAGCTC	150
	GGCAAGGGCT	CTTTCAAGTA	TGCGCTGGTT	CTTGACAAAGT	TGAAGGCCGA	200
20	GCGTGAGCGT	GGTATCACCA	TTGATATCGC	CCTCTGGAAG	TTCGAGACCC	250
	CCAAGTACTA	TGTCACCGTC	ATCGATGCC	CCGGCCATCG	TGATTTCATC	300
	AAGAACATGA	TTACTGGTAC	TTCCCAGGCC	GATTGCGCCA	TTCTCATCAT	350
	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGCCAGA	400
	CCCGTGAGCA	CGCTCTCCTC	GCCTACACCC	TCGGTGTGAA	GCAGCTCATC	450
25	GTCGCCATCA	ACAAGATGGA	CACCACAAA	TGGTCCGAGG	CCCGCTTCAA	500
	CGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	550
	CCAAGACTGT	TGCCTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAAACATG	600
	CTTGAGGCTT	CCACCAACTG	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGGT	650
	CAAGGGTGGC	AAGGCTACTG	GCAAGACCC	CCTCGAGGCC	ATCGACTCCA	700
30	TCGAGCCCCC	CAAGCGTCCC	ACCGACAAGC	CCCTCCGTCT	TCCCCTTCAG	750
	GACGTTTACA	AGATCGGCGG	TATCGGCACA	GTCCTGTG	GCCGTATCGA	800
	GACTGGTATC	CTCAAGCCCG	GTATGGTCGT	TACCTTCGCC	CCTTCCAACG	850
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACACAGAGCA	GCTCTCTGAG	900
	GGTGTCCCCG	GTGACAACGT	TGGTTCAAC	GTGAAGAACG	TCTCCGTCAA	950
35	GGAAATCCGC	CGTGGCAACG	TTGCCGGTGA	CTCCAAGAAC	GACCCCCCTC	1000
	TTGGCGCCGC	TTCTTTCGAT	GCCCAGGTCA	TCGTCCTCAA	CCACCCCGGC	1050
	CAGGTGGTG	CTGGTTACGC	CCCCGTCTC	GATTGCCACA	CTGCCACAT	1100
	CGCCTGCAAG	TTCGCTGAGC	TCCTGCAGAA	GATCGATCGC	CGTACTGGTA	1150
	AGGCTGTTGA	GGAGAGCCCT	AAGTTCATCA	AGTCTGGTGA	TGCTGCCATC	1200
40	GTCAAGATGA	TTCCCTCCAA	GCCCCATGTGC	GTTGAGGCTT	TCACTGAGTA	1250
	CCCTCCCCCTC	GGTCGTTTCG	CTGTCCGTGA	CATGCGTCAG	ACCGTCGCTG	1300
	TCGGTGTCAT	CAAGAAGGTC	GAGAAGGCCG	CTGCTGGTTC	CGGCAAGGTC	1350
	ACCAAGTCCG	CTGCCAAGGC	TGGTGGCAAG	AAATAAA		1386

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2) INFORMATION FOR SEQ ID NO: 1997

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*
 (B) STRAIN: 000
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

10	ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT	50
	CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGC GGTTG	100
	GTATCGACAA GCGTACCATC GAGAAGTTG AGAAGGAAGC CGCTGAGCTC	150
	GGCAAGGGTT CCTTCAAGTA TGCCTGGTT CTTGACAAGC TCAAGGCCGA	200
15	GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTGAGACTC	250
	CCAAGTACTA CGTCACCGTC ATCGATGCC CCGGCCATCG TGATTCATC	300
	AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT	350
	TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGCCAGA	400
	CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC	450
20	GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCAGG CTCGTTTCGA	500
	GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC	550
	CCGCCACCGT CGCTTCGTC CCCATCTCCG GCTTCAACGG CGACAAACATG	600
	CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC	650
	CAAGGCCGGC AAGTCCACTG GCAAGACCC CCTCGAGGCC ATCGACGCCA	700
25	TTGAGCAGCC CAAGGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG	750
	GATGTCTACA AGATCGGCCG TATCGGCACA GTGCCCGTCG GCCGTATCGA	800
	GACTGGTGTGTC CTCAAGCCCG GTATGGTGT TACCTTCGCT CCTTCCAACG	850
	TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG	900
	GGTGTCCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA	950
30	GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG	1000
	TCGGCGCTGC CTCTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT	1050
	CAGGTCGGTG CCGGCTACGC TCCCCTCCTC GATTGCCACA CTGCCACAT	1100
	TGCCCTGCAAG TTCGCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA	1150
	AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC	1200
35	GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTGAGGCTT TCACCGACTA	1250
	CCCTCCCCCTC GGTGCTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG	1300
	TCGGTGTCAAT CAAGGCCGTG GACAAGACCC AGGCTGTCGC TGGCAAGGTC	1350
	ACCAAGTCTG CTGCCAAGGC TGCCAAGAAC TAA	1383

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2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414
 (C) ACCESSION NUMBER: Z23012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5	ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT	50
	CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCCTG	100
	GTATCGACAA GCGTACCAT T GAGAAGTTCG AGAAGGAAGC CGCCGAAC	150
	GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA	200
10	GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC	250
	CCAAGTACTA TGTCACCGTC ATTGACGCTC CCGGCCACCG TGACTTCATC	300
	AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT	350
	CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCAAAG GATGCCAGA	400
	CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC	450
15	GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA	500
	GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTCAACC	550
	CCAAGGCCGT TGCTTCGTC CCCATCTCCG GCTCAACGG TGACAACATG	600
	CTCACCCCCCT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC	650
	CAAGGCTGGC AAGTTCACCG GCAAGACCC CTTGAGGCC ATCGACTCCA	700
20	TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG	750
	GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA	800
	GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG	850
	TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTGCTGAG	900
	GGCCAGCCTG GTGACAACGT TGGTTCAAC GTGAAGAACG TTTCCGTCAA	950
25	GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCC	1000
	TGGCGCCGC TTCTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGC	1050
	CAGGGTCGGTG CCGGCTACGC CCCCGTCCTC GACTGCCACA CTGCCACAT	1100
	TGCCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA	1150
	AGGCTACCGA GTCTGCCCTC AAGTTCATCA AGTCTGGTGA CTCCGCCATC	1200
30	GTCAAGATGA TCCCCCTCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA	1250
	CCCTCCCCTG GGTCCTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG	1300
	TCGGTGTATC CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC	1350
	ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA	1383

35

2) INFORMATION FOR SEQ ID NO: 1999

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT

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29

2) INFORMATION FOR SEQ ID NO: 2000

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000

CCACCYTCIC TCAMGTTGAA RCGTT

15 2) INFORMATION FOR SEQ ID NO: 2001

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001

ACYACITTRA CIGCYGCYAT YAC 23

30

2) INFORMATION FOR SEQ ID NO: 2002

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002

CCIGARGARA GAGCIMGWGG T 21
45

2) INFORMATION FOR SEQ ID NO: 2003

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

2) INFORMATION FOR SEQ ID NO: 2004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAAACCA	CATTGACTGC	TGCTATCACC	AAAGTTTAG	100
CCGAACAAAGG	TGGTGCCAAC	TTCTTGGATT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGGTTGTG	TTTGTCAACA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTGGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTCGATGA	ACACATTCCA	600
ACTCCATCAA	GAGACTTGG	ACAACCATT	TTGTTACCA	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAACCTGTTG	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTGTTAAGA	GGTGTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAAGA	AGTTCTTGGC	TTCTTGTAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAACTAACGA	TGTCACTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGGTTGGTGA	1100
ATTGATCAA	TCTTGTCCAT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTGA	TTTGATTTAT	GCCATGTGGA	CTTGTAGAGA	TATCCTTCTC	1350
AAACTTCTTG					1360

2) INFORMATION FOR SEQ ID NO: 2005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Schizosaccharomyces pombe*
 (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

AAGCCGCATG	TCAATATTGG	TACTATTGGT	CATGTTGACC	ACGGTAAAC	50
GACGTTGACG	GCTGCTATT	CTAAATGCCT	TTCTGATCTT	GGTCAAGCTA	100
GTTTTATGGA	TTATAGTCAA	ATTGACAAGG	CCCCCGAGGA	AAAGGCACGT	150
GGTATTACCA	TTTCATCTGC	CCATGTTGAA	TACGAAACTG	CTAATCGTCA	200
CTATGCCCAT	GTGGATTGTC	CTGGTCACGC	CGATTACATT	AAGAATATGA	250
TTACTGGTGC	TGCTACAAATG	GATGGCGCTA	TCATTGTTGT	TTCTGCTACC	300
GATGGTCAAA	TGCCTCAAAC	TCGTGAACAT	TTGCTTCTGG	CTCGTCAAGT	350
CGGTGTAAAG	CAAATTGTTG	TATACATCAA	TAAAGTCGAT	ATGGTCGAGC	400
CTGATATGAT	CGAGCTTGTC	GAAATGGAAA	TGCGTGAGCT	ACTCTCCGAA	450
TACGGATTG	ATGGTGACAA	TACTCCAATT	GTAGCGGCA	GTGCTTATG	500
TGCCTTAGAG	GGTCGTGAGC	CTGAGATTGG	TCTCAATAGT	ATTACTAAAT	550
TGATGGAAGC	TGTTGATAGT	TATATTACTC	TTCCCTGAAAG	AAAAACGGAT	600
GTCCCTTTCT	TGATGGCCAT	CGAGGACGTT	TTTCAATT	CAGGTCGCGG	650
AACTGTAGTC	ACTGGCCGTG	TCGAGCGCGG	TACTTTAAAG	AAGGGTGCTG	700
AAATCGAAAT	CGTCGGTTAT	GGTAGCCATT	TAAAGACTAC	CGTTACTGGA	750
ATTGAAATGT	TCAAAAAGCA	GCTTGATGCC	GCCGTTGCCG	GTGACAATTG	800
TGGCCTTTA	CTTCGTTCTA	TCAAGCGAGA	GCAATTAAA	CGTGGAATGA	850
TTGTCGCTCA	ACCAAGAAC	GTTGCTCCTC	ATCAGAAATT	CAAGGCATCA	900
TTCTATATTT	TGACAAAAGA	GGAAGGAGGT	CGTCGTACCG	GTTCGTTGA	950
CAAGTATCGT	CCCCAACTGT	ACAGTCGTAC	TTCCGACGTT	ACTGTCGAAC	1000
TTACCCACCC	TGATCCTAAC	GACTCAGACA	AAATGGTTAT	GCCTGGAGAC	1050
AATGTCGAGA	TGATCTGTAC	GCTTATTTCAC	CCCATTGTCA	TCGAAAAGG	1100
ACAACGCTTC	ACAGTTCTGT	AGGGTGGAAAG	CACTGTAGGC	ACAGCTTTGG	1150
TTACTGAACT	TTTGGATTAG	TGCATTTATG	AACTTATTGG	CTTTAAAAT	1200
TTTGCATGCT	GAATAACCAAT	ATTATGTCCC	TTCTCAGAAT	TCTATAACTA	1250
CAGTGTCAATT	ATTGTAATAA	GACTTTGCA	TCCATTGACA	ATGGTATTG	1300
ATACTTTAT	AGTTTCTACT	ATTGTTAGCC	AAAGTTATAA	AA	1342

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1046

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: KMK107
- (C) ACCESSION NUMBER: AF027199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

ATGAGTATTTC AACATTTCCG	TGTCGCCCTT ATTCCCTTT	TTGCGGCATT	50
TTGCCCTTCCT GTTTTGCTC	ACCCAGAAAC GCTGGTGAAA	GTAAAAGATG	100
CTGAAGATCA GTTGGGTGCA	CGAGTGGGTT ACATCGAAC	GGATCTCAAC	150
AGCGGTAAAGA TCCTTGAGAG	TTTCGCCCC GAAGAACGTT	TTCCAATGAT	200
GAGCACTTT AAAGTTCTGC	TATGTGGTGC GGTATTATCC	CGTGGTGACG	250
CCGGGCAAGA GCAACTCGGT	CGCCGCATAC ACTATTCTCA	GAATGACTTG	300
GTTAAGTACT CACCAGTCAC	AGAAAAGCAT CTACGGATG	GCATGACAGT	350
AAGAGAATTA TGCAGTGCTG	CCATAACCAT GAGTGATAAC	ACTGCTGCCA	400
ACTTACTTCT GACAACGATC	GGAGGACCGA AGGAGCTAAC	CGCTTTTTG	450
CACAAACATGG GGGATCATGT	AACTCGCCTT GATCGTTGGG	AACCGGAGCT	500
GAATGAAGCC ATACCAAACG	ACGAGCGTGA CACCACGACG	CCTGCAGCAA	550
TGGCAACAAAC GTTGCACAA	CTATTAACGT CGGAACACT	TACTCTAGCT	600
TCCCGGCAAC AATTAATAGA	CTGGATGGAG GCGGATAAAAG	TTGCAGGACC	650
ACTTCTGCGC TCGGCCCTTC	CGGCTGGCTG GTTATTGCT	GATAAATCTG	700
GAGCCAGTGA GCGTGGGTCT	CGCGGTATCA TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT CCCGTATCGT	AGTTATCTAC AGCACGGGGA	GTCAGGCAAC	800
TATGGATGAA CGAAATAGAC	AGATCGCTGA GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA A			861

2) INFORMATION FOR SEQ ID NO: 2011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: CLSiS L-491
- (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

ATGAGTATTTC AACATTTCCG	TGTCGCCCTT ATTCCCTTT	TTGCGGCATT	50
TTGCCCTTCCT GTTTTGCTC	ACCCAGAAAC GCTGGTGAAA	GTAAAAGATG	100
CTGAAGATCA GTTGGGTGCA	CGAGTGGGTT ACATCGAGCT	GGATCTCAAC	150
AGCGGTAAAGA TCCTTGAGAG	TTTCGCCCC GAAGAACGTT	TTCCAATGAT	200
GAGCACTTT AAAGTTCTGC	TATGTGGTGC GGTATTATCC	CGTGGTGACG	250
CCGGGCAAGA GCAACTCGGT	CGCCGCATAC ACTATTCTCA	GAATGACTTG	300
GTTAAGTACT CACCAGTCAC	AGAAAAGCAT CTACGGATG	GCATGACAGT	350
AAGAGAATTA TGCAGTGCTG	CCATAACCAT GAGTGATAAC	ACTGCGGCCA	400
ACTTACTTCT GACAACGATC	GGAGGACCGA AGGAGCTAAC	CGCTTTTTG	450
CACAAACATGG GGGATCATGT	AACTCGCCTT GATCGTTGGG	AACCGGAGCT	500
GAATGAAGCC ATACCAAACG	ACGAGCGTGA CACCACGATG	CCTGCAGCAA	550
TGGCAACAAAC GTTGCACAA	CTATTAACGT CGGAACACT	TACTCTAGCT	600

TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTAAATTGCT	GATAAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCCGGGATTA	TTAAACCGCC	CTTCCGCGG-MR-HEG-ATGTCAGAGG	GATAGATCCA	49
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2) INFORMATION FOR SEQ ID NO: 2013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACCGGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCGG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCGTTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GTAGATGGTC	AAGGTAACCT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

2) INFORMATION FOR SEQ ID NO: 2014

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

AGCTCCTATC	TGGATTATGC	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	50
AGATGTCCGA	GATGGCCTGA	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	100
TGAACGTACT	AGGCAATGAC	TGGAACAAAG	CCTATAAAA	ATCTGCCC GT	150
GTCGTTGGTG	ACGTAATCGG	TAAATACCAT	CCCCATGGTG	ACTCGGCGGT	200
CTATGACACG	ATCGTCCGCA	TGGCGCAGCC	ATTCTCGCTG	CGTTATATGC	250
TGGTAGACGG	TCAGGGTAAC	TTCGGTTCTA	TCGACGGCGA	CTCTGCGGCG	300
GCAATGCGTT	ATACGGAAAT	CCGTCTGGCG	AAAATTGCC	ATGAAC TGAT	350
GGCCG					355

2) INFORMATION FOR SEQ ID NO: 2015

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAACCT CAAAAACATC TG

22

2) INFORMATION FOR SEQ ID NO: 2016

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC AWACAGCCAT

20

2) INFORMATION FOR SEQ ID NO: 2017

- (i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

GTAGCTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2021

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAACTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2028

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACAAATCACG

20

2) INFORMATION FOR SEQ ID NO: 2029

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

2) INFORMATION FOR SEQ ID NO: 2030

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

2) INFORMATION FOR SEQ ID NO: 2031

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACCA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2035

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACCA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2036

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACCA CTGGTTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2037

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2038

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

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2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

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2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

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GTTCTTCCTC CGTATCGTC

19

2) INFORMATION FOR SEQ ID NO: 2046

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATT TTCTATCTAT

20

2) INFORMATION FOR SEQ ID NO: 2047

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2160 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: CS109
 - (C) ACCESSION NUMBER: Z49094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCAGGAGGA	GTTCAGGTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGTT	AGAACAAAAA	GCAACAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCCTGCT	TACATGGATA	ATTACCTCAA	GGAAAGTCATC	AATCAAGTTG	850
AAGAAGAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

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AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCGA	950
TCAATACGTC	TCTTACCCCTG	ACGATGATT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AACTTGGTGC	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTCCG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAG	1400
TAACACAACT	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAAATGG	1450
CTGCTGCCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCTTGTG	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTCTGT	ATTTAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAAC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCAGGAGGA	GTTCCTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTGG	250
TTAAGGCAAT	CGTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTCAAC	TTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGTT	AGAACAAAAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGGAAC	TATGGAATGC	550

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AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTA	600
CCTCAGTTAG	CCTTGTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCATTCA	CATCCAGAAG	CAGCCCAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTCGG	AATTAAACCA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTGGAGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCCGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTACAC	TACTCAAATG	CCATTCAAG	1400
TAACACAAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCCTT	GCAAATGGTG	GAACTTACTA	TAACCAATG	1500
TATATCCATA	AAAGTGTCTT	TAGTGTATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAACT	CGTGCATGA	AAGAAACGAC	ACGCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAACGT	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACTAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATAACC	AGAGGGGCTC	TACAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGTCTGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTT	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTG	GTTATCGCAG	CCATTGTCTT	AGGCAGGAGGA	GTTCAGGAGG	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAT	CAACTCATTG	CTGACTTGAG	200

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TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AAACAAGAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950
TCAATACGTC	TCTTACCCCTG	ACGATGATT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAAT	1150
ACGGTGTAA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAG	1400
TAATACAACA	GAATCTAATA	AAACAATACGG	AGCAAGTAGT	GAAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCATGA	AGGAAACGAC	ACCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTGACT	TATGGAAC	GGCGTGGAGC	CTATCTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTG	1800
AATCGTTAA	CTCCTATCGT	TGGAGATGGT	TTCTTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTG	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAAC	TCGATCAATA	CGTCTCTTAC	CTGACGATGA	50
TTTGCAGTC	GCATCTACGG	TCGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAA	ACTTG	AGCTCGTCAC	CAAGCAAGTA	ACGTTTCATT	150
CAAGCTGTGG	AAACCAATCG	TGACTGGG	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AATA	ACGGTGT	TTATGATTCC	250
TGGTTAATGA	TATT	ACTATCCGG	GAACAAGCAC	ACCTGTCTAC	300
AACTGGGATA	GAGC	CGGTAATATT	ACTCTGCAAT	ATGCTCTTC	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTCCTT	AATGGTCTT	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTC	AAGTAATACA	ACAGAATCTA	ATAAACAAATA	500
CGGAGCAAGT	AGTGA	TGGCTGCTGC	TTATGCTGCC	TTTGC	550
GTGGCACTTA	CTATAAACCA	ATGTATATCC	ATAAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTT	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GGAAGTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATAC	TCGAAATCGT	850
TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	TAACTCCTAT	CGTTGGAGAT	900
GGTTTCC	TTGCAGCTAA	AGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATA	AGACGAATA	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TTGTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAA	CTTG	AGCTCGTCAT	CAAGCAAGTA	ATGTTTCATT	150
CAGGCTGTGG	AGACCAATCG	TGACTGGG	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCC	GCTT	AATATGGAGT	CTATGACTCT	250
TTGTACATGA	TGTT	CCTT	AACTATCCTG	GCACTGATAC	300
AACTGGGATC	ATGT	ACTT	TGGAAACATT	ACAATCCAGT	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTCCTT	AATGGTCTT	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTC	AAGTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGA	TGGCTGCTGC	TTATGCCGCC	TTTCTAATG	550
GTGGTATT	TA	ATGTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGA	AA	TGATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AAATGATGAA	AACTGTTTA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT ATACTGACGA CGAAATTGAA AAGTATATCA AGAACACTGG	800
CTACGTAGCT CCAGATGAAA TGGTTGTGG TTATACTCGT AAGTATTCTA	850
TGGCTGTATG GACTGGTTAC TCAAATCGTT TAACCTCAAT CGTAGGAGAT	900
GGTTTCCTAG TTGCTGCTAA GGTTTATCGC	930

2) INFORMATION FOR SEQ ID NO: 2052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAACGTA	TATTCCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAACAAAG	GTTGGTTAG	ATCGAGCCAA	AACTTTCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACTATGCTA	ACGCCATTTC	AAGTAATACA	450
ACAGAATCTA	ACAAACATTA	CGGTGCAAGT	AGTAAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATT	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGT	GGTAGTGAGA	AAGAATTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAACCTCAAT	TGTTGGAGAT	GGTTTCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAACTCACCT	GCTCCACAC	AACCCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAAATCAGA	ATCCCTCAACC	AGCAC	1195

2) INFORMATION FOR SEQ ID NO: 2053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 17619
- (C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCAGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTCACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTC	AACTAACACA	ACCGAATCAG	ACAAAAAATA	500
TGGAGCAAGT	AGTAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAAGTCGT	CTTTAGTGTAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCCTCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAAAATAC	AGTTGATTC	300
GTTGAT					306

2) INFORMATION FOR SEQ ID NO: 2055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAAC	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATT	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATT	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACC	GT AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTCG	TATGTCACAG	AACTGGAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCC	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCCCTCCC	CATAATTAG	550
CTGAGGTCA	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTCA	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCCGCTGGT	TGTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTCC	TATGAAATCA	ATAAGGCCAA	800
TCTAGTCAAG	AAAATCGATG	ATGTTCGTGT	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACCTAAC	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACTT	TAATATGGTG	GCGATTGACA	1000
ATTTCACACC	TCGTCAGGTT	GGGATTGTT	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAAGTAT	TTTGGCGCGT	TCACGCTT	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTCGAAGG	TTTGATTGCGT	GTGATTTCGA	1150
TTTGGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTGCAAC	TGTACCGTT	GACCAATACC	GATGTGGTTG	1300
TCTTGCAGGA	AGAAGAAGCA	GAGCTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTGAGT	TCTTACAAG	1450
ACACTGCGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCAGTCC	1550
ACGTTCC	CGGGCTTCCA	CCTTGGAAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTGTTCAA	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTCACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTATGTGG	AAGTACTGGA	TCAGTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCACTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTTAGC	AGTGGCTCCG	1950
ATTAAGACTAG	ATGATGTTGT	CTTGGTTAGT	CAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTTC	CGGTTGTCGG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGAAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCCTGA	GTTGAAAAC	AAACCGCATT	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTGTT	TGGCGATTTC	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTCTGACA	CGATTTCAGA	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAAT	AA			2472

2) INFORMATION FOR SEQ ID NO: 2056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTT	150
CATTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCC	TGCAACAAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACTAC	TCAAATGCCA	TTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAAG	600
TCGTCTTAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGC	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCTA	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAAGAAC	CTGGTTACGT	AACTCCAGAT	GAAATGTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CACTTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTGTTATT	AAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

2) INFORMATION FOR SEQ ID NO: 2057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAACGCTAA	AAACATCTGT	GGGATATTAA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAAC	GGGATAAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTGCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAGT	500
AATACGACTG	AGTCACACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAATGGC	550
TGCTGCTTAC	GCTGCTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATA	AGATGATGAA	800
ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GAATATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTAAC	1150
TACTCCAAGC	ACGAATAATA	GTGAAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

2) INFORMATION FOR SEQ ID NO: 2058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTAAA	AACATCTGTG	GGATATTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTCTA	100
ACGGGAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACC GTGACT	GGGGTTCTGC	200
CATGAAGCCA	ATCACAGACT	ATGCT CCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTT	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAAC TG	GGATAAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGT CGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AA GTACGGAG	CAAGTAGTGA	GAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	CGCATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAA ACTA	800
CATCAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTT	GTTGGTTATA	850
CTCGCAAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TCGAAGTGGT	GAGTCGTCT	TTAAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTCACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAAACAAAT	AATACCAATA	ACCAGCAACC	AAATACAACG	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

2) INFORMATION FOR SEQ ID NO: 2059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAA	150
CGCCATTTC	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TTAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTCT	GATGCCGGTA	CTCGGGCTAT	GAAAGAAACT	ACTGCCTATA	350

TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATA CGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTCGTTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTGG	550
ACAG					554

2) INFORMATION FOR SEQ ID NO: 2060

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAACG	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCTT	CGGAATTAAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTCACGA	TGAGCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	450
ACCGCGCCAA	GACTTCTTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTC	AAAGTAACACA	ACCGAACATCAG	ACAAAAAAATA	550
TGGAGCAAGT	AGTAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTTA	CTATAAACCA	ATGTATATCC	ATAAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	AAAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTAAA	AATGGTGTCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

2) INFORMATION FOR SEQ ID NO: 2061

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAACACTGCA	50
ATTTCCTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTCGC	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTG	CGTCTGCAAT	TTGCATTTTT	500
CCTTAGCAA	TCTCAGAACG	GTCTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

2) INFORMATION FOR SEQ ID NO: 2062

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1216 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTAAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCGTACG	ATGATTGCA	AGTCGCATCT	ACGGTCTGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAAAC	TTGGTGTCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACCTGG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAAGTAGTGAA	AAAATGGCTG	CTGCCTACGC	550
TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTAG	TGATGGTAGC	GAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACGT	700
TTTAACCTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAAC	CTGGTTACGT	AGCTCCAGAT	GAAATGTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTGCTG	GTAAAGTCTA	TCGTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGTAT	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

2) INFORMATION FOR SEQ ID NO: 2063

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATAACGTCTC	TTACCCCTGAC	GATGATTG	AAGTCGCATC	CACGGTCGTA	50
GATGTTCAA	ATGGTAAAGT	CATGCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATT	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACTG	GGATCGAGCA	TATTTTGGTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTTGG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATT CGC	AAACGGCGGT	ATT TACCACA	AAACCAATGTA	550
CATCAATAAG	GTTGCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTCTGACC	600
CTGGCACAAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAAC TG	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAACTATACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTT	800
GTAGGGTATA					810

2) INFORMATION FOR SEQ ID NO: 2064

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

TCTTACCCCTG	ACGATGATT	GCAAGTCGCA	TCTACGGTCG	TAGATGTTTC	50
AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	GCAAGTAACG	100
TTTCATTG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	CTGGGGATCA	150
ACTATGAAAC	CAATCACAGA	CTATGCTCCT	GCCTTGGAGT	ACGGTGTCTA	200
CGATTCAACT	GCTACTATCG	TTCACGATGA	GCCCTATAAC	TACCCCTGGGA	250
CAGATATCCC	TCTCTATAAC	TGGGATCGAG	CATATTCGG	TAATATTACT	300
CTGCAATATG	CCCTTCAACA	ATCTCGAAC	GTACCTGCCG	TTGAAACACT	350
AAACAAGGTC	GGTCTAGATA	AGGCTAAAAC	CTTCCTTAAT	GGTCTTGGTA	400
TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAG	TAATACAAC	450
GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAAATAG	CTACCGCCTA	500
TGCCGCATTC	GCAAATGGTG	GTATTTACCA	CAAACCAATG	TACATCAATA	550
AAGTTGTCTT	TAGCGATGGT	AGCGAAAAAG	AATTTTCTGA	CCCTGGCACA	600
AGAGCCATGA	AAGAAACGAC	TGCTTACATG	ATGACAGAAA	TGATGAAAAC	650
AGTCTGGACG	TACGGAACTG	GTCGTGGTGC	CTACCTGCCT	TGGCTTCCTC	700
AAGCTGGTAA	AACAGGTACC	TCTAACTATA	CTGACGAAGA	AATTGAAAAG	750
TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GA		782

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

2) INFORMATION FOR SEQ ID NO: 2067

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

2) INFORMATION FOR SEQ ID NO: 2068

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAAC

19

2) INFORMATION FOR SEQ ID NO: 2069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

2) INFORMATION FOR SEQ ID NO: 2070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTCGCTAACG	TGCGCGAAC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTG	TTCGAGTGGC	TGATCGGTTC	200
GCCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AAACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTCGTT	CTCTGACCC	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGG	GCTCCACTGT	400
TCGTCACCGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTC	TGGGTGACTT	CCCGATGATG	ACCGAGAAGG	GCACGTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGGTCAG	CCAGCTGGTG	CGGTCGCCCG	550
GGGTGTACTT	CGACGAGACC	ATTGACAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCGA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAAACCGG	700

1074

TCACCGTGCT	GCTCAAGGCG	CTGGGCTTGA	CCAGCGAGCA	GATTGTCGAG	750
CGGTTGGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCAG	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTC	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCGC	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAACGTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTG	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGCACGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTAGC	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCAACCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCGCGCGAT	CAAGGAGTTC	TTCGGCACCA	1300
GCCAGCTGAG	CCAATTCTATG	GACCAGAAC	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTCGGC	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCCGC	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCGATCGA	AACCCCTGAG	GGGCCAAC	TCGGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCC GTT CCGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGGTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTGCGC	GATCGATGCG	1650
GACGGTCGCT	TCGTGAGCC	GCGCGTCTG	GTC CGC CGC A	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGG	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCCTTCCT	GGAGCACGAC	1800
GACGCCAAC	GTGCCCTCAT	GGGGCAAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGCGATCGA	CGCGGCGACG	TCGTCGTCG	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCGG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGT	CAACCACGGC	ACTTGCGCCA	2050
ACCACTGCCC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTCAAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAAC	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTCGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCC	GAATCTCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGC	ATCGGTGCCG	AGGTTCGCGA	CGGGGACATC	2400
CTGGTCGGCA	AGGTCA	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGC	TCGGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCGCTGAA	GGTGC	GGCGAATCCG	GCAAGGTGAT	CGGCATT	2550
GTGTTTCCC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGC	TATG	AGAAACGCAA	GATCTCGAC	GGTGACAAGC	2650
TGGCGGCCG	GCAC	AAAGGGCGTGA	TCGGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGT	CGACGGCACC	CCGGTGGACA	TTATT	2750
CACCCACGGC	GTG	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTG	AGCGGCTGGA	AGGTCGACGC	CGCCAAGGGG	2850
GTTCCGGACT	GGG	GCTGCCGAC	GAAC	AGGCGCATGC	2900
GAACGCCATT	GTG	CGGTGTTCGA	CGGCGCCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTT	ACGCTGCCA	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGG	CATGCTCTC	GACGGGCGCA	GCGCGAGCC	3050
GTTCCCGTAC	CCGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGG	CGA	CACGCCCGT	CCACCGGGCC	GTACTCGATG	3150
ATCACCCAGC	AGCC	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGT	CCATGCAGGC	CTACGGTGC	GCCTACACCC	3250
TGCAGGGAGCT	GTT	AAGTCCGATG	ACACCGTCGG	CCGCGTCAAG	3300
GTGTACGAGG	CGAT	GGGTGAGAAC	ATCCC	CGGGCATCCC	3350
CGAGTCGTT	AAGG	TCAAAGAAC	GCAGT	TGCCTCAACG	3400
TCGAGGTGCT	ATCG	GGTGC	TCGA	CGAAGGTGAG	3450
GACGAGGACC	TGG	CGCGGCCAAC	CTGGG	ATCTGTCCC	3500
CAACGAATCC	GCAAG	AGGAT	GTAA		3534

2) INFORMATION FOR SEQ ID NO: 2073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2074

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2075

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

2) INFORMATION FOR SEQ ID NO: 2076

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTCA GATTACCCA RGCGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 2080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

2) INFORMATION FOR SEQ ID NO: 2081

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

2) INFORMATION FOR SEQ ID NO: 2082

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

2) INFORMATION FOR SEQ ID NO: 2083

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACCGTCAA CACCCGTACA AGTCGTCTT TGCGCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAAACATAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 2087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

2) INFORMATION FOR SEQ ID NO: 2088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

2) INFORMATION FOR SEQ ID NO: 2089

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAAC TATTGACCTT

20

2) INFORMATION FOR SEQ ID NO: 2090

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAACCTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAAACTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

2) INFORMATION FOR SEQ ID NO: 2094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTCT TGACCTACTT TCAA

24

2) INFORMATION FOR SEQ ID NO: 2095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

2) INFORMATION FOR SEQ ID NO: 2096

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

2) INFORMATION FOR SEQ ID NO: 2097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082

- (A) ORGANISM: *Mycoplasma pneumoniae*
- (B) STRAIN: ATCC 29342
- (C) ACCESSION NUMBER: AE000019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

ATGGCAAGAG	AGAAATTG	CCGATCTAAA	CCCCACGTTA	ATGTAGGTAC	50
TATTGGCCAC	ATTGACCACG	GTAAAACAAC	TTAACAGCA	GCTATTTGTA	100
CTGTATTAGC	AAAAGAAGGT	AAATCAGCTG	CTACTCGTTA	CGACCAAATC	150
GATAAGGCTC	CGGAAGAAAA	AGCACGGGGA	ATTACGATTA	ACTCCGCTCA	200
CGTGGAGTAC	TCCTCTGACA	AGCGTCACTA	TGCTCACGTT	GAATGTCCAG	250
GACACGCTGA	CTACATTAAG	AACATGATTA	CTGGTGCTGC	ACAAATGGAT	300
GGTGCCATT	TAGTAGTTTC	AGCAACTGAC	AGTGTATGC	CCCAAACCCG	350
TGAACACATT	TTGTTGGCCC	GCCAAGTGGG	TGTGCCACGC	ATGGTAGTGT	400
TCCTAAACAA	GTGTGACATT	GCAACTGATG	AAGAAGTGCA	AGAGTTAGTA	450
GCAGAAGAGG	TACGTGACTT	ATTAACCTCT	TACGGCTTTG	ATGGCAAGAA	500
CACCCCTATT	ATTATGGTT	CTGCACCTAA	AGCGCTTGAA	GGTGATCCTA	550
AGTGGGAAGC	TAAGATCCAT	GATTTAATGA	ATGCAGTTGA	TGAATGGATT	600
CCAACCTCTG	AACGTGAAGT	GGACAAACCC	TTCTTGTTGG	CAATCGAAGA	650
CACCATGACG	ATTACTGGCC	GTGGTACCGT	GGTTACCGGT	CGGGTTGAAC	700
GTGGTGAATT	GAAAGTAGGT	CAAGAAATTG	AAATCGTTGG	TTTACGTCCA	750
ATCCGTAAAG	CAGTTGTTAC	CGGAATCGAA	ATGTTCAAAA	AGGAACATTGA	800
TTCAGCAATG	GCTGGGGACA	ACGCTGGGT	ATTACTCCGT	GGTGTGGACC	850
GTAAAGAAGT	GGAACGTGGT	CAAGTGTAG	CTAAACCAGG	TTCGATTAAA	900
CCGCACAAAGA	AATTAAAGC	GGAAATCTAT	GCTTTAAGA	AGGAAGAAGG	950
TGGTCGTAC	ACCGGTTTCT	AAACGGTTA	CCGTCCCCAA	TTCTACTTCC	1000
GTACTACAGA	CGTTACTGGT	TCGATTTCCC	TACCAAGAAA	CACCGAAATG	1050
GTGCTACCAAG	GTGACAATAC	CTCGATTACA	GTGAACTAA	TTGCACCAAT	1100
TGCTTGTGAA	AAAGGTAGTA	AGTTCTCCAT	CCGTGAAGGT	GGTCGAACGG	1150
TTGGTGCTGG	TTCAGTCACG	GAAGTGCTG	AATAG		1185

2) INFORMATION FOR SEQ ID NO: 2098

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

2) INFORMATION FOR SEQ ID NO: 2099

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGCGAC	GACCCGGACC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCGGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTCGCCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCCAGCCC	CATTGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCCGAGCC	350
AGGTTTCCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCAGGCCT	TCATGCCACG	GGGGCCCCGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTGAG	CGCCGTTCGC	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTTGGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCACTTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCAGGCCG	AGCCGAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCA	TTCCACACCC	TGCGGCACGT	800

1084

ACACGTCTTT	ATGTAGCGCG	ACATAACCTGC	TGCGCAATT	GTAGGGCGTC	850
AATAACACCCG	CAGCCAGGGC	CTCGCTGCC	AGAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCCAGTGC	950
GAAAGTTCCC	GCCGAAAATC	GCAGCCACGT	TACGCTCGTG	GACATACC	1000
TTTCGGCCCG	GCCGCGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTCTGAT	CCCCTTCAGT	CCTGGTTACC	1100
GGAGGAAACC	GGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTCACGGCGG	TAGAAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTCAA	1300
CGCCGGCTA	TCCGCGGACG	CATTCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGCGTTCGG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTCGGTCGAA	TGATATTCAT	1450
AGGTTCGGTC	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGC	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTCGC	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCACTCCC	1750
GGTCGACGGC	GGCATGGGT	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATT	TGTTTAGCGG	AATCATCACC	1850
GACTCGTCGA	TCGCGTTCA	CATCGCACGG	GTAGCCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGGGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACCTCGA	CGTGCAAAAC	2000
GAGGAGCACC	TGGCCAGCTT	GGCCGGCCGG	GTGACCGAGG	CGATCGGGGC	2050
GGGAAACAAG	CTCGACGGGG	TGGTGCATT	GATTGGGTT	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCCG	GAGGTTCCAT	CGTCGGCATG	GAATTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACCTGGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGGCGCGC	GAGGCCGGCA	AGTACGGTGT	2350
GCGTTCGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGGCAGGCCG	GTCGCAAGA	CGGTGTGCGC	GCTGCTGTCT	GACTGGCTGC	2550
CGCGACAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCCG	GCACACCCAA	2600
TTGCTCTAG					2609

2) INFORMATION FOR SEQ ID NO: 2102

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

2) INFORMATION FOR SEQ ID NO: 2103

1085

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCGAGCG GAAATAGTTG GAC

23

2) INFORMATION FOR SEQ ID NO: 2104

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CICGAGTC

18

2) INFORMATION FOR SEQ ID NO: 2105

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3297 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT	GCGCGAGCAG	ACGCAAAGC	ACCCCAAATC	GGGCGATT	TT	50
GGGGGCTTTT	GCGTCTGCTC	GCGGGACGCG	CTGGGTGGCC	ACCATGCCG		100
GGCTGATTGG	CTTTGTGTTG	TCGGTGGCGA	CGCCGCTGCT	GCCCCTCGTG		150
CAGACCACCG	CGATGCTCGA	CTGGCCACAG	CGGGGGCAAC	TGGGCAGCGT		200
GACCGCCCCG	CTGATCTCGC	TGACGCCGGT	CGACTTTACC	GCCACCGTGC		250
CGTGCACGT	GGTGCACGCC	ATGCCACCCG	CGGGCGGGGT	GGTGCTGGGC		300
ACCGCACCCA	AGCAAGGCAA	GGACGCCAAT	TTGCAGGGCGT	TGTCGTCGT		350
CGTCAGCGCC	CAGCGCGTGG	ACGTCACCGA	CCGCAACGTG	GTGATCTTGT		400
CCGTGCCGCG	CGAGCAGGTG	ACGTCCCCGC	AGTGTCAACG	CATCGAGGTC		450

1086

ACCTCTACCC	ACGCCGGCAC	CTTCGCCAAC	TTCGTCGGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCGC	550
AGATTGTCGG	GGTGTTCACC	GACCTGACCG	GGCCCGCGCC	GCCCAGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCAG	750
CTCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TCGCCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTCGGCTT	CCTGCTCTGG	CATGTATCG	GCGGAATT	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTT	CGCTGGTCG	GCAGCCCCGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCGC	CGGGCTAGTG	TGCTGGCTGC	TGCTGTCGCG	1100
TGAGGTGCTG	CCCCGCCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGGATGCC	GTTCAACAAC	1200
GGCCTGCCGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGCGCTGG	1300
CCGTCGTTAC	CGCCGCATTC	ACACTGGGTG	TGCAAGCCAC	CGGCCTGATC	1350
GCGGTGGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGGT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTGGTGTGCG	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCCGTCA	1500
ACGGTGTGG	AAGCCACCAG	GGTCGCGCC	AAAATGGGC	CGAGCCAGGC	1550
GTGGTATAACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGTTTCGCT	GTCGCGGCCG	TTCGGCTTTT	TGATCACCGC	GCTATGCTG	1650
TTCACCGCGG	TGTTCATCAT	GTTGCGCGC	AAGCGAATT	CCAGCGTGGC	1700
CCGCGGACCG	CGCTGGCGGC	TGATGGCGT	CATCTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCACC	AAGTGGGTGC	ACCACTTCGG	GCTGTCGCC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTGG	TATCCCCATC	1850
GGTGTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCCTGGCG	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCCTC	1950
AGCTACGGTC	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTCG	CCCTGTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGT	GCCGGTTCA	TGGCGCGGT	2150
GTTCGTCGCG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTCGAGCC	TGATACCAAT	GCGGGTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCTT	GGGGCCCCCTT	GGGCCGCTG	GGTGGAGTC	2350
ACCCGGTCGG	CTTCACGCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCAA	CCAGCCCCG	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGT	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCCG	GGCGGATGGT	2750
GCCCGACGAC	CTATACGGAG	AGCAGCCAA	GGCGTGGCGC	AACCTGCGCT	2800
TCGCCCAGAC	AAAGATGCC	GCCGATGCCG	TCGGGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCCTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCC	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCGCGACTG	GGCCCGCGAT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCCTG	GTCGATGCC	CTCCCGCCCA	GCTCGAGTTG	GGCACCGCGA	3250
CCCGCAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

2) INFORMATION FOR SEQ ID NO: 2106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C
2) INFORMATION FOR SEQ ID NO: 2107

31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCACGCTC GC

32

2) INFORMATION FOR SEQ ID NO: 2108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTTGGTTAC AACCCGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCAGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCAGGGCCCTT AACGATTTCGA GCGAATCTGG ATTCAAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCAGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCAGGGCTTGA TGAAGTTTG GGTTTCCTTG ACAATTGCC CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

1089

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCAGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCAGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCAGGGCTTGA TGATTTCTCTC GAATCTAGAT TGGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2116

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCAGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCGC

39

1090

2) INFORMATION FOR SEQ ID NO: 2117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCGC

36

2) INFORMATION FOR SEQ ID NO: 2118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCTGTATCTG TTCTTGGCCC GC

42

2) INFORMATION FOR SEQ ID NO: 2119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCCCTAAGG CTGTTCCATT CGTTGCCCGC

40

2) INFORMATION FOR SEQ ID NO: 2120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCAGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCC C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

2) INFORMATION FOR SEQ ID NO: 2124

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

2) INFORMATION FOR SEQ ID NO: 2125

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACCGGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

2) INFORMATION FOR SEQ ID NO: 2126

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

2) INFORMATION FOR SEQ ID NO: 2127

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1093

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

22

2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TGCCTTG

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2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTAA TATCTAAAGA AGAGTTAATA AACTCGCAT ATAGCATTAG	50
ACCAAGAGAA AATGAGTATA AACTATACT AACTAATTAA GACGAATATA	100
ATAAGTTAAC TACAAACAAT AATGAAAATA AATATTTGCA ATTAAAAAAA	150
CTAAATGAAT CAATTGATGT TTTTATGAAT AAATATAAAA CTTCAAGCAG	200
AAATAGAGCA CTCTCTAAC TAAAAAAAAGA TATATTAAAA GAAGTAATT	250
TTATTAAAAA TTCCAATACA AGCCCTGTAG AAAAAAATT ACATTTGTA	300
TGGATAGGTG GAGAAGTCAG TGATATTGCT CTTGAATACA TAAAACAATG	350
GGCTGATATT AATGCAGAAT ATAATATTAA ACTGTGGTAT GATACTGAAG	400
CATTCTTAGT AAATACACTA AAAAAGGCTA TAGTTGAATC TTCTACCACT	450
GAAGCATTAC AGCTACTAGA GGAAGAGATT CAAAATCCTC AATTGATAA	500
TATGAAATTT TACAAAAAAA GGATGGAATT TATATATGAT AGACAAAAAA	550
GGTTTATAAA TTATTATAAA TCTCAAATCA ATAACCTAC AGTACCTACA	600
ATAGATGATA TTATAAAGTC TCATCTAGTA TCTGAATATA ATAGAGATGA	650
AACTGTATTA GAATCATATA GAACAAATTG TTTGAGAAAA ATAATAGTA	700
ATCATGGGAT AGATATCAGG GCTAATAGTT GTTTACAGA ACAAGAGTTA	750
TTAAATATTG ATAGTCAGGA GTTGTAAAT CGTGGAAATT TAGCTGCAGC	800

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ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCACT	CTGATTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCCT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAACT	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	AAAATTCTT	CATGATTCAT	1300
TATTTAATTG	AGCTACCGCA	AAAAACTCTA	TGTTTTAAC	AAAATAGCA	1350
CCATACCTAC	AAAGTAGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTC	ATAAATTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAAG	CATCAGATT	AATAGAATT	1500
AAATTCCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAA	ATATCAATT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGG	TCTCTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAATA	CTGCCCTCGA	AAAAAACTAT	TTATTAAATA	ATAAAATTCC	1700
ATCAAACAAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTATTT	1800
TCTAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAAATATAG	GATACCTGAA	AGATTTAAA	ATAAGGAAA	AGTAAAAGTA	1950
ACCTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTGCTAG	2000
ATTAAGTGTA	GATTCACTTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAAGTAAACTT	ACTTGGATGT	2100
AATATGTTA	GTTATGATTT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACCTCT	GGCTCACTCA	GGTAAATGGA	TAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTGATT	2350
CTATAGATAA	TAAGCTAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	AAAAAATTAG	AGCCTGTTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	AAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTGAAAGAT	ATCTAAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAAA	2750
AGAAATTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACGCAG	CATTCTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACTATTAG	TACAGGTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATT	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTAA	TCATTTGTCT	GAATCTAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTAAT	AATAATTCCA	AAAAACTAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCC	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTGTT	3700
GGGAAACTGG	AGCAGTTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAAC	3750
AGATTACTTG	ATTCAATAAG	AGATTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAAAATT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAACTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTTCATT	3950
TGATGGAGCA	GGAGGAACCT	ACTCTTATT	ATTATCTTC	TATCCAATAT	4000
CAACGAATAT	AAATTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAGGAAA	4100
GTAAATAAAA	GATGTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAAACAATA	GATTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATT	GTTTAATAAT	4250
AGAAATAAAT	CTTGTGCAA	AATCTTATAG	TTTGTATTG	TCTGGGGATA	4300
AAAATTATT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGGAGCTA	TATCTAAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTAA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTC	TCTATTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTGTGAA	AATTTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTGG	CAATATAAGT	TTCTGGAAT	TGTTTGGGTT	TGAAAATATA	5200
AATTTGTAA	TCGATAAAATA	CTTACCCCTT	GTTGGTAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTGTC	ACAATAATAA	AAATATAGAT	ATATATTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTAATAAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACAA	AAAAAGTAAA	TATAAATTAA	GATAGTTCTT	5600
CTTTTGAGTA	TAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTAAAG	5750
ATATTAAAAA	ACTATCATT	GGATATATAA	TGAGTAATT	TAAATCATT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATT	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTAAATGGTA	GTAGATACTA	CTTGATACT	6000
GATACCGCTA	TTGCCCTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTGAT	AGTGATTGTC	TAGTGAAT	AGGTGTGTT	AGTACCTCTA	6100
ATGGATTGAA	ATATTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACCTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTG	6250
ATAGAAAAAA	ATATTACTTT	AATACTAAC	CTGCTGAAGC	AGCTACTGG	6300
TGGCAAACTA	TTGATGGTAA	AAAATATTAC	TTAACCTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	AAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTA	TGGTAAACAT	6450
TTTATTGTTA	ATACTGATGG	TATTATGCA	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATT	GAATATTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTAC	CAAAATGAAT	TCTTAAC	GAATGGTAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAACCTAA	TAATGCTATT	GCTGCAATT	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTCT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTAAAGGA	CCTAATGGAT	6850
TTGAGTATT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAAC	TTGAATGGCA	AAAAATATTA	6950
TTTGATAAT	GACTCAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACATATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACAA	7150
CTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTGAAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTAA	CTTGAATGG	TAAAAAAATAT	7350
TACTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATT CCTATA	TTTACATGAC	AATATATATT	ATTTGGTAA	7700
TAATTCAAAA	CGGGCTACTG	GTTGGGTAAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAATT	TTTACTTTAG	AAATGGTTA	CCTCAGATAG	GAGTGTAA	7850
AGGGTCTAAT	GGATTGAAAT	ACTTTGCACC	TGCTAACAAAC	GATGCTAACAA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCT	ACATTTACTT	7950
GGAAAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATT	CTTTGGTGT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

2) INFORMATION FOR SEQ ID NO: 2130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTA CAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATT	AAAATAAAAA	150
GATATAAATA	GTTTAACAGA	TATTTATATA	GATACATATA	AAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTAAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACCTCAG	TTGAGAAAAA	TTTACATTT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTT	TATGATAGTA	400
ATGCATTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTAT	GATAAACAGA	550
AAAATTCAT	AAACTACTAT	AAAGCTCAA	GAGAAGAAA	TCCTGAACCT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAAACTTTG	AAGAATTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAC	CTAGTCAGT	AACAGTGGAT	TTTGGGAAA	TGACAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAA	GTAGTTTGAA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATT	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	AAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTAT	GATGGAAC	1350
GGAAAGTATT	TAAGAGTTGG	TTCTTCCC	GATGTTAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCCGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTGAA	TAGAAGCTGA	TTTAAGAAC	1500
TTTGAATCT	CTAAAACAA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTGACG	ATGCAAGAGC	AAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTGAA	GGTTCTCTT	GTGAAGATGA	TAATCTTGAT	1650
TTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTCAG	AGAGAGGATA	TATACACTAT	ATTGTTCA	1750
TACAAGGAGA	AAAATTAGT	TATGAAGCAG	CATGTAAC	TTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTCAGAAA	AATATAGAAG	ATTCAAGAA	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATAC	GATATATTG	CAGGTTTGAA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTAAAG	2050
AGGATATTTC	TCCTAAGTCA	ATAGAAATAA	ATTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAA	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAAT	TATTGGATCA	TTCTGGTGA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTCAT	CAAAAGAATA	TATATCATT	AATCTAAAG	2350
AAAATAAAAT	TACAGTAAA	TCTAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGTATTG	AACTAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTCA	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATT	AACTCTGAC	2550
TCTATTAATT	ATATAAAAGA	TGAATTAAA	CTAATAGAAT	CTATTCTGA	2600
TGCACTATGT	GACTAAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTA	2650
TATCTTTGA	GGACATATCA	GAGACTGATG	AGGGATTAG	TATAAGATT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATT	GTAGAAACTG	AAAAACAAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTCT	AAGATAAAAG	2800
GTACTATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAACT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAAACAG	CTACAAC	AATCATTACT	TCATCTTGG	3250
GGATAGCTAG	TGGATTAGT	ATACTTTAG	TTCCCTTAC	AGGAATTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTACTTC	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCATTTAGT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATT	3450

GTGATATCAG	AAATAGATT	TAATAATAAT	TCAATAGTTT	TAGGTAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTTGTCAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTA	AGAAGCTTAG	AAAATGATGG	CACAAAACGT	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTTATT	GGAGATATT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAAT	TTAGATAGTA	ATACTAGAAG	TTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCTTTCTA	3950
TGGTCAGGA	GGAACTTATG	CATTGTCCT	TTCTCAATAT	AATATGGGT	4000
TAAATATAGA	ATTAAGTGAA	AGTGTGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAACAT	AGAATCTGAT	AAAATTAAA	AAGGTGATT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAA	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGT	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTCCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTAAATTCA	AATCATATT	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	AAAAAATATA	CCATATAGCT	TTGTTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAAATGG	TTCAACAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTTCTTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTGTA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTGTACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATT	AGATGAAAGT	GGAGTAGCTG	AGATTTGAA	4700
GTTCATGAAT	AGAAAAGGT	ATACAAATAC	TTCAAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATT	TCGTTAATT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATT	ATAATAAGT	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTCATTAA	GTAAATACAA	CTAGAAACTA	ATTATACTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTCTC	TCAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	GTAAATAAA	GTTGTAATT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCGT	ATATGAAACA	AATAATACCT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAAATGA	AAAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTACAA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATT	ATATTAATAA	CTTGGAAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTG	GACTGTAGGC	GATGATAAAAT	ACTACTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCATTG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATC	GATTTAAATA	TTTGCCTTCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAAAT	ATTGACGAAA	5800
ATATTTATTA	TTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTGCCTTCA	GAACACAGGT	AAGCTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAAAC	CTATTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATT	6050
CTACTTGCT	GAACACGGAG	AAATGCAAAT	AGGAGTATT	AATACAGAAG	6100
ATGGATTTAA	ATATTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATT	TGGTATATT	AATTCATAA	ATAAAATTAA	6200
CTATTTGAT	GATTCAATT	CAGCTGTAGT	TGGATGGAAA	GATTAGAGG	6250
ATGGTTCAAA	GTATTATTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAACCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATT	AATTGATGAT	ATAAAATATT	ATTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AAATAATTATT	ACTTTAATGA	6800
GAATGGTGA	ATGCAATTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTGGTGA	AGATGGTGT	ATGCAGATTG	GAGTATTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTGCACA	TCAAATACT	TTGGATGAGA	ATTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTCAAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

2) INFORMATION FOR SEQ ID NO: 2131

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAAATTG GAAAG

25

2) INFORMATION FOR SEQ ID NO: 2132

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

2) INFORMATION FOR SEQ ID NO: 2133

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 bases
 - (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACATTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

2) INFORMATION FOR SEQ ID NO: 2137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCGGTC	100
AGGTAGGCCT	TCCGTACATC	GTGGTCTTCC	TGAACAAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCCG	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAC	TGGTAGAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTCCG	450
GTTCAAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACACC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCTGCTG	550
GCGAGAACTG	CGGCCTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGCAA	GCCAGGTTCG	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTAAC	GCGAACTGCC	GGAAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTCA	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCAGTC	GTACCGTCG		889

2) INFORMATION FOR SEQ ID NO: 2138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGAGC	CCGAGCTGCT	GGAACCTGGTC	GAGATGGAAG	TTCGCGATCT	200
GCTAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTG	CGGAGGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTCGGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGC	ACCATCAAGC	CGCACACCAA	650
GTTCGAGTGC	GAAGTGTACG	TGCTGTCAA	GGAAGAAGGT	GGTCGTACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCAGT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCCGTAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

2) INFORMATION FOR SEQ ID NO: 2139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTCACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTGTTAG	AAAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTGTT	CCTGTTGGTG	250
AGAAAAGTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTG	GATCGATGAA	300
GGTGAAGAAA	TTTCTTCGA	TAAAAAATGG	GCAATTCTATA	GAGATCCACC	350
AGCTTTGAA	GATCAAAGCA	CAAAAAGTGA	GATTTTGAA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAAGTGT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAAG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTCACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACCTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTGC	950

TCACCTAGAT	GCTACAACGG	TTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAAC	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
GAAAAATTCT	TATCACACC	ATTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTACAAGG	TAAATATGAT	CATTTACCAAG	AAAATGCTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAGCG	GATAAATTAA	AAGGTTAA	1398

2) INFORMATION FOR SEQ ID NO: 2140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTAAGTTA	600
CCTCAGTTAG	CCTTGTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCGTCT	TACATGGATA	ATTACCTCAA	GGAGGTACATC	AATCAAGTAG	850
AACAAGAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCGA	950
TCAATAACGTC	TCTTACCCCTG	ACGATGATTT	GCAAGTCCGA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTGTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTGCGTCTT	CAGTGACGGT	AGTAAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTGGCA	TACGGAACTG	GTCGTGGAGC	CTATCTCCC	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTG	1800
AATCGTTAA	CTCCTATCGT	TGGAGATGGT	TTCTTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTGT	ATTCAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAAACCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
					2157

2) INFORMATION FOR SEQ ID NO: 2141

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

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2) INFORMATION FOR SEQ ID NO: 2142

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

2) INFORMATION FOR SEQ ID NO: 2143

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTAAA	CACCCAGAAT	GAAATATCAG	CATTTGGAA	50
TACTCAAAG	ATATTAAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTGTTTT	TTATGACGGC	CCCCCAACTG	CAAATGCCCT	TCCTCATGCT	150
GGCCATGTT	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAACAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAAGTTGA	ATTAGAGGTT	AAAAAAAAAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAAATT	ATAAAATGAAT	GTAAAAAAAG	350
TGTATTAAAT	TATGAAAAAG	AATGGCGGGA	TTTTCTAAA	GATTAGGAT	400
ACTGGGTTGA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAGA	TTTATCAGCT	600
GTTGTTAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCCT	CCCTGGACTT	TGCCTGCAA	TGAGCATTA	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATT	TATAATAACT	GAAAATACG	AAATTATTGA	800
TACCTTTCA	GGAAAGTAATT	TAATTAATT	AAAATACATT	CCTCCTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTCAT	ATAGCACCAG	CTCATGGGA	950
AGATGACTAC	CAATTGGTT	TAGAGCGTGA	TTGGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGTTAAT	1050
AAAGCTAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAAACAA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGA	1150
GATGTGGTAA	TCCTTGATA	TATTATGCGA	TGGAAGGTTG	GTATTATTAA	1200
ACAACTAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTC	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGAAAC	ACCATTAAAT	1350
GTATGGATT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTGGTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTT	TGATAACCAG	AAAATTTTA	1600
ATCAAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTT	ACAGTTTACT	AGTAATTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTG	TTTAAGATGG	GCCTTAATT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATT	ATAAATTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTA	ATAAAAGAAA	2050
GTAATATT	TGTAAATAAT	TACGATTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTGAGAGG	2150
ACGATTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTAAACA	ACTTTATCAA	GACTAGTGGC	TCCATTGTT	2250
CCATTTATAT	CTGAAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAATG	CAGATTAAA	AATTAAGCAA	CCTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAACAA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTCTT	CTGTGGGACC	2600
AAAACCTAGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAaaaaaaAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATT	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAATT	ATCTCCTGAA	TTAATTGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAAATT	AAGAAAAAAAG	AAAATTTAC	CAATAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAACGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCATTTA	ATAATAAAGA	3050
AATAAAATT	TCCTTATTAT	ATTAA			3075

2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTGAGG	CATTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTTATCC	GGCCTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTCACCCCT	TGTTACACCG	TTTCCATGA	GCAAACGTAA	300
ACGTTTTCAT	CGCTCTGGAG	TGAATACCAAC	GACGATTTC	GGCAGTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTAA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTGA	TTTAAACGTG	GCCAATATGG	ACAACCTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCA	GTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGCGTAA					660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCA

22

2) INFORMATION FOR SEQ ID NO: 2149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

2) INFORMATION FOR SEQ ID NO: 2150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: K12
- (C) ACCESSION NUMBER: X53796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTGCCT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTCACCT	GATCTCCGG	GCTGTTAAC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAAC	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCA	ATTGTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTGAC	450
GGATTTAAC	TGAACATCAC	CGGAAATGAT	GATTATTTG	CCCCGGTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCCGGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTT	600
ATTAATAACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAACTC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexineri*
- (C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA CAAAATTG A TGAAAAAAT TGGGTTGCC GTGAGCATTT	50
TGAGTTTAT CGGCATCGTT TACCATGTGG TTTAGCTTA ACAAGCAAAA	100
TTGATATCAC GACGTAAAAA AAGTCATTGG ATGATTCA GC GTATAAGTTT	150
TATCCGGTAA TGATCTATCT GATTGCTCAG GCCGTGAATC AATTGATGA	200
GTTGAGAATG GCGATAAAAG ATGATGAATT GATCGTATGG GATTCA GTCG	250
ACCCACAATT CACCGTATT CATCAAGAAA CAGAGACATT TTCAGCACTG	300
AGTTGCCCAT ACTCATCCGA TATTGATCAA TTTATGGTGA ATTATTTATC	350
GGTAATGGAA CGTTATAAAA GTGATACCAA GTTATTTCC CAAGGGTAA	400
CACCAAGAAA TCATTAAAT ATTCAGCAT TACCTTGGGT TAATTTGAT	450
AGCTTTAATT TAAATGTTGC TAATTTACC GATTATTTG CACCCATTAT	500
AACAATGGCA AAATATCAGC AAGAAGGGGA TAGACTGTTA TTGCGCTCT	550
CAGTACAGGT TCATCATGCA GTTGTGATG GCTTCCATGT TGACGCTTT	600
ATTAATCGGC TACAAGAGTT GTGTAACAGT AAATTAAAAT AA	642

2) INFORMATION FOR SEQ ID NO: 2154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTAG AGTTAGGAC

20

2) INFORMATION FOR SEQ ID NO: 2155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

2) INFORMATION FOR SEQ ID NO: 2156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG AAAAAATTGA TAAAATAGT TGGAACAGAA AAGAGTATTT	50
TGACCACTAC TTTGCAAGTG TACCTTGAC ATACAGCATG ACCGTTAAAG	100
TGGATATCAC ACAAAATAAG GAAAAGGGAA TGAAACTATA TCCTGCAATG	150
CTTTATTATA TTGCAATGAT TGTAAACCGC CATTCAAGAGT TTAGGACGGC	200
AATCAATCAA GATGGTGAAT TGGGGATATA TGATGAGATG ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTTAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAT	GCTCCGGAAA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTC	AGAAAGGATA	TGATTATTTG	ATTCCTATT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTTACAC	TTTGCCGTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAAATAG	TTAA			624

2) INFORMATION FOR SEQ ID NO: 2157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

2) INFORMATION FOR SEQ ID NO: 2158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAAGTTCT A

21

2) INFORMATION FOR SEQ ID NO: 2159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACCTTA ATAAAATTGA TTTAGACAAT TGGAAGAGAA AAGAGATATT	50
TAATCATTAT TTGAAACCAAC AAACGACTTT TAGTATAACC ACAGAAATTG	100
ATATTAGTGT TTTATACCGA AACATAAAAC AAGAAGGATA TAAATTTAC	150
CCTGCATTTA TTTTCTTAGT GACAAGGGTG ATAAACTCAA ATACAGCTT	200
TAGAACTGGT TACAATAGCG ACGGAGAGTT AGGTTATTGG GATAAGTTAG	250
AGCCACTTTA TACAATTTT GATGGTGTAT CTAACACATT CTCTGGTATT	300
TGGACTCCTG TAAAGAATGA CTTCAAAGAG TTTATGATT TATACCTTC	350
TGATGTAGAG AAATATAATG GTTCGGGGAA ATTGTTCCC AAAACACCTA	400
TACCTGAAAA TGCTTTTCT CTTTCTATTA TTCCATGGAC TTCATTTACT	450
GGGTTTAACT TAAATATCAA TAATAATAGT AATTACCTTC TACCCATTAT	500
TACAGCAGGA AAATTCAATT AATAAGGTAATCAATATAT TTACCGCTAT	550
CTTACAGGT ACATCATTCT GTTGTGATG GTTATCATGC AGGATTGTTT	600
ATGAACCTCA TTCAGGAATT GTCAGATAGG CCTAATGACT GGCTTTATA	650
A	651

2) INFORMATION FOR SEQ ID NO: 2160

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTGAACAC TATTTAACCC AGC

23

2) INFORMATION FOR SEQ ID NO: 2161

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

2) INFORMATION FOR SEQ ID NO: 2162

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTA ATATTATCAA ATTAGAAAAT TGGGATAGAA AAGAATATTT	50
TGAACACTAT TTTAACCGC AAACCTACGTA TAGCATTACT AAAGAAATTG	100
ATATTACTTT GTTTAAAGAT ATGATAAAAA AGAAAGGATA TGAAATTAT	150
CCTTCTTGAT TTTATGCAAT TATGGAAGTT GTAAATAAAA ATAAAGTGT	200
TAGAACAGGA ATTAATAGTG AGAATAAATT AGTTTATTGG GATAAGTTAA	250
ATCCTTGTAT TACAGTTTT AATAAGCAAA CTGAAAATT TACTAACATT	300
TGGACTGAAT CTGATAACAA CTTCACTTCT TTTTATAATA ATTATAAAAA	350
TGACTTGCTT GAATATAAAG ATAAAGAAGA AATGTTTCCT AAAAACCGA	400
TACCTGAAAA CACCATACCG ATTTCAATGA TTCCCTGGAT TGATTTAGT	450
TCATTTAATT TAAACATTGG TAACAATAGC AACCTTTAT TGCCTATTAT	500
TACGATAGGT AAATTTTATA GTGAGAATAA TAAAATTAT ATACCAGTTG	550
CTTGCAGCT TCATCATGCT GTATGTGATG GTTACCATGC TTCATTATTT	600
ATGAATGAAT TTCAAGATAT AATTCTATAAG GTAGATGATT GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGGCATCC	TGAACACGAC	GCCCGCTATG	150
ATCCAACCTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTGTT	CCGCTCTCAG	ACAGAACATCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTCGC	TTTCCGTCTA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAAC	400
GTCCTGAGGG	TGTCGTATC	TACGGCCTTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCAATTA	CTTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACCGGCCGAT	CTGTCTTGCC	GATCTTCGCG	AGTCCGGCTT	TTTGGGTTTA	650
CACTGTCGGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTCTCGA	700
CGGCTCCCCG	TGTGCTCAT	GGCCAAGCGG	AATATTCCGA	GATCGGATTC	750
AGCTTTGCCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTTT	800
CGCGAAGTCC	TTTGTGTCGA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGGTTGC	GGAGCGGTCC	TGTTGGGGAT	CGGCGAACTT	900
TACGGCTCGC	CGTCATTCCCT	CACCTTCATC	CTACCGATGT	GGGTTGTCGC	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTTGGCAG	1000
AGTCGACGA	CATCGCGGGA	TCAGCGGTGCG	CGTTCTACTT	CTGCATCCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAACCGG	1100
CGATACAGCG	TGGCCCGTGA	TTTGTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

2) INFORMATION FOR SEQ ID NO: 2166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

18

1115

2) INFORMATION FOR SEQ ID NO: 2167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

2) INFORMATION FOR SEQ ID NO: 2168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

2) INFORMATION FOR SEQ ID NO: 2169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

2) INFORMATION FOR SEQ ID NO: 2170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAAT CTTCGAAC TG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CT

24

2) INFORMATION FOR SEQ ID NO: 2177

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCCCT GCTGCCTATC GAAGACGTGT TCCCGTGCC

49

2) INFORMATION FOR SEQ ID NO: 2178

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCCTG CTGCCTATCG AACGTGCC

38

2) INFORMATION FOR SEQ ID NO: 2179

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC

39

2) INFORMATION FOR SEQ ID NO: 2180

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC

15

2) INFORMATION FOR SEQ ID NO: 2181

- (i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC	50
ACATCCTGCT GAGCCGTCAAG GTTGGCGTTC CTTACATCAT CGTGTTCCTG	100
AACAAGGCCG ACATGGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT	150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCCTGGC GACGACACCC	200
CGATCATCAA GGGTTCGGCC AAACCTGGCTC TGGAAAGGCGA CGAAGGCCCA	250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT	300
TCCTACGCCT GAGCGTGCCG TTGACGGTAC GTTCCTGATG CCTGTTGAAG	350
ACGTGTTCTC GATCTCCGGC CGTGGTACGG TTGTGACCGG TCGTATTGAG	400
CGGGGCATCA TCAAGGTCTGG CGAAGAAATC GAAATCGTGG GTATCAAAGA	450
CACGGTCAAG ACCATTGTA CCGGCGTTGA AATGTTCCCGC AAACGTCTGG	500
ACCAGGGCGA AGCTGGCGAT AACGTCGGTC TGCTGCTGGC TGGTACCAAG	550
CGTGAAGACCG TGGAACGTGG TCAAGTTCTG GCCAAGCCAG GCTCGATCAA	600
GCCACACACT GACTTCGACG CCGAGGGTGT AATTCTGTCC AAAGAAGAAG	650
GTGGTCGTCA CACTCCTTTC TTCAAGGGCT ACCGTCTCA GTTCTACTTC	700

1120

CGTACAACGT	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
GGTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
TCGCCATGGA	AGAAGGT				817

2) INFORMATION FOR SEQ ID NO: 2184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTGTTC	AGTGGGTGGG	GTGCAGCCTC	AAAGTAAAC	AGTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTA	ATAAAATGGA	150
TAGAACCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCC	TAATCGATCT	TGTAACTATG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATTCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAACG	AGTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATT	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAGT	CTTTCTATCG	500
TTCCCTATGCT	TTGCGGTACA	GCCTTTAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTGGCTTA	TTTACCAAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGAA	TATGAAGACG	GCACAGAAAGT	TTCTGTAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACCTTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTAG	AAAGCGGTT	750
TTATGCTTAT	AACTCAACCA	AAGATAAAA	AGAAAGAATT	GGTCGTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACTAT	CATTCAGGT	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGAA	1150
GCTGAAGTGG	GACAACTCA	AGTTGCTTAT	CGTAAACACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAT	ACGCTAACGA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTGT	ACGACATCAA	AGGTGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTC	AAGAAGCATT	GCAAAATGGT	GTGTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

2) INFORMATION FOR SEQ ID NO: 2185

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 820 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Succinivibrio dextrinosolvens*
 - (B) STRAIN: ATCC 19716

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCCT	ACCATAACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATAAACGGC	GAAGAGAAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACC GGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAACCTGG	CGTTGAAATG	TTCCGTAAAGT	TACTAGACGA	500
AGGTCTGCA	GGTGATAACG	TTGGTGTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAACGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 2186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACCGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

2) INFORMATION FOR SEQ ID NO: 2187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

CAGTGGGTGG	GGTGCAGCCT	CAAAGTAAA	CAGTTGGAG	ACAAGCAAAT	50
AAATATGGTG	TTCCAAGAAT	AGTATTGTA	AACAAAATGG	ATAGAACCGG	100
TGCAAATTTC	TACAATGTAG	AAGATCAAAT	TCGCAACCGT	TTAAAAGCTA	150
ATCCAGTTCC	ACTTCAAATT	CCAATCGGTG	CTGAGGATAA	TTTTAAAGGC	200
GTAATCGATC	TTGTAACAT	GAAAGCTTTA	GTGAGGAAAG	ATGATACTAA	250
GCCAACGGAT	TATGTAGAAA	AAGAAATTCC	AGCTGAACCTT	AAAGAAAAGG	300
CAGAAGAATA	TCGCACAAAA	ATGATAGAAG	CAGTTTCTGA	AACTTCAGAT	350
GAGTTGATGG	AAAAATATT	AGGCGGAGAA	GAATTAAGCC	TTGAAGAGAT	400
TAAAACAGGG	ATTAACAGCAG	GATGTTTAAG	TCTTCTATC	GTTCCTATGC	450
TTTGCAGGTAC	AGCGTTAAA	AATAAAGGGG	TCACACCTTT	ACTTGATGCT	500
GTTGTGGCTT	ATTTACCAAGC	TCCTGATGAA	GTGGCAAATA	TCAAGGGTGA	550
ATATGAAGAT	GGCACAGAAG	TTTCTGTAAA	ATCAACTGAT	GATGGCGAGT	600
TTGCAGGACT	TGCATTTAAA	ATTATGACAG	ATCCATTGTT	AGGACAACCTT	650
ACTTTCGTGC	GTGTTATCG	CGGTTGTTA	GAAAGTGGTT	CTTATGCTTA	700
TAACCTCAACT	AAAGATAAAA	AAGAAAGAAT	TGGTCGTTTG	TTAAAAATGC	750
ACTCTAACCA	AAGAGAAGAG	ATTAACAGTGC	TTTACGCAGG	CGAAATTGGT	800
GCTGTTGTTAG	GACTTAAAGA	TACTTTAACAA	GGGGATACTC	TTGTAAGTGA	850
AAAAGATAAG	GTAATCCTTG	AAAGAATGGA	TTTCCAGAT	CCAGTTATTT	900
CTGTTGCAGT	TGAGCCAAA	ACTAAAGCAG	ATCAAGAAAA	AATGTCTATT	950
GCTTTAAATA	AATTAGCACA	AGAAGATCCA	AGTTTTAGAG	TTTCTACAGA	1000
TGAAGAAAGT	GGCCAAACTA	TCATTTCAAGG	TATGGGTGAG	TTACACCTTG	1050
AAATTATCGT	TGATAGAATG	CTTCGTGAAT	TTAAAGTTGA	AGCTGAAGTA	1100
GGTCACCAC	AAGTTGCTTA	TCGCGAAACT	ATTAGAAAAA	CTGTTGAACA	1150
AGAATACAAA	TACGCTAAC	AATCAGGTGG	TCGTGGTCAG	TATGGACATG	1200
TATTCTTACCG	CCTTGAACCA	CTTGAGGCCAG	GTAGTGGATA	TGAATTGTT	1250
AATGATATCA	AAGGTGGAGT	AATTCCAAA	GAATACATTG	CTGCAGTTGA	1300
TAAAGGTGTT	CAAGAAGCAT	TACAAAATGG	TGTTTTAGCA	GGTTATCCTG	1350
TGAAAGATGT	TAAAGTAAC	GTAAATGATG	GAAGTTATCA	CGAGGTGGAT	1400
TCATCTGAGA	TGGCGTTAA	ACTTGCTGCT	TCTATGGGCT	TTAAAGAAGG	1450
TGCTAGAAA	GCAGGTGCTG	TGATCTTAGA	GCCTATGATG	AAAGTTGAAG	1500
TAGAAACTCC	TGAAGATTAC	ATGGGTGATG	TTATTGGAGA	TCTTAACAAA	1550
CGCCGTGGTC	AAGTAAATAG	CATGGATGAG	CGTGGTGGAA	ATAAAATCAT	1600
CACAGCATT	TG				1612

2) INFORMATION FOR SEQ ID NO: 2188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTC	GTGGGTGGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATAA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGTG	CAAATTCTA	CAATGTAGAA	GATCAAATTG	GCAACCGTT	200
AAAAGCTAAT	CCAGTTCCAC	TTCAAAATTCC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCCT	AATCGATCTT	GTAACTATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAACG	CAACGGATTA	TGTAGAAAAA	GAAATTCCAG	CTGAACCTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTCCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAAA	TAAAGGGTT	CAACCTTGTC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAAGCTC	CTGATGAAGT	GGCAAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTAAAAT	CATGACAGAT	CCATTGTAG	700
GACAACCTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAAA	GAAAGAATTG	GTCGTTGTT	800
AAAAATGCAC	TCTAACAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCCTATTGC	TTTAAATAAA	TTAGCACAAG	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAACATATC	ATTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAACCAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTGTTAA	TGATATCAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCCCT	1350
GCAGTTGATA	AAGGTGTTCA	AGAACCATTA	CAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTC	GAAGATGTTA	AAGTAACGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATTC	ATCTGAGATG	GCGTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAAATAGCA	TGGATGAGCG	TGGTGGAAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGCG	ACCGCATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCGGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCGAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACCTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGTT	750
ACCAAGCCGAC	GCTTGGCGAG	GATCTTGGCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCCTGCC	950
GTGAACCCGC	TGGAGTGCAG	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTGCGGTG	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCCCT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 2190

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGCAG	CATCTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAA	100
CGACGGATCT	CCTCAAACGT	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCGGTTC	CTGTGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCGAGC	GGGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGAAAA	ATTGGCCTCT	TTGGGGTGC	GGGTGTGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGT	CGGTCAAGATG	AACGAGCCC	CAGGTGCCG	TGCGCGTGT	600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTATCG	ACAATATTT	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTCTG	GGTCGTATT	CCGCCGCTGT	TGGCTACCAG	750
CCTACCCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACTGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA	950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCTAA	GTTGGTGAAG	TTCCTCTCCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCTTTCT	GGTCTCCTCA	TGGGTACG	1248

2) INFORMATION FOR SEQ ID NO: 2191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGT	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGT	ATTCAGCTCG	ACGGCGAATC	CAAGGTGTCT	CTTGTGTTCG	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGT	CCCGTGTCCG	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTCC	GTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

2) INFORMATION FOR SEQ ID NO: 2192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania panamensis*
- (B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGCAGCAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTGACCGGG	150
CGGCAACATC	TCCGTGCCGG	TGGGCCGGA	GACGCTGGGC	CGCATCTTC	200
ACGTGCTGGG	CGACCGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTG	GCGGTGCCGG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCGAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCCTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGC	CGCATCCC	CCGCCGTGGG	750
TTACCAGCCG	ACGCTGCGG	AGGATCTTGG	CATGCTGCAG	GAGGCATTA	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCGCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTT	1150
CTGTCGCAGC	CGTTCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATT	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGAAA	TAGGCCCGAG	ACTCGTGAGC	ACTTGTGCT	100
TGCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCGA	TGACCCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTACT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCAAG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTCGTGG	TATGGTCATC	GCTGCCCTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAAC	ACCGCCCCA	GGCTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTGTA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTCCTCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
					912

2) INFORMATION FOR SEQ ID NO: 2194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCG	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACGCC	AGCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAACCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTCCTGGCC	GTGTTGAGCG	400
TGGTACCCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCCTC	GTCTCCATGT	ACGTCCTGAC	CAAGGAGGAG	650
GGTGGTCGTC	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
					887

2) INFORMATION FOR SEQ ID NO: 2195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCAA	ATGTAGGACT	CTTGCAGCGG	ACTGACTGAT	TGGGGGAAAT	50
CCATTTTTTC	TTTTTCTTT	TTCTTTTGGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAAGGCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAAGAT	CGTCGTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAACATAAG	GAGATGTTGG	AGCTTGTGGA	GTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTCGAG	GGTGAGGAAA	CGCCCACATCAT	CTTCGGTTCT	300
GCCCTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCCG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAAACCGA	TATCGAAACC	TTCAAGAAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAACT	CTGGCCTTTT	GTTGCGTGGT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTG	TTCTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAAC	750
GGATTCCGCC	AAAATATCG	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTCCCTG	900
ACGCAGCGAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

2) INFORMATION FOR SEQ ID NO: 2196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTCAGA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCCAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATAACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGCCG	TGTCGAGCGA	GGTGTCTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTG	GACAAGTCAA	GGCCCACAAG	600
AAGTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAGA	TGCTCACGAC	750
AAGCTTGTGA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
	GCCACA				806

2) INFORMATION FOR SEQ ID NO: 2197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTC	AGCGAATTGT	50
CGTCTTGTC	AACAAGGTG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTCGAGAT	GGAGATGCGC	GAGCTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTACATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTC	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCCTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

2) INFORMATION FOR SEQ ID NO: 2198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
- (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT CAGATGCCCG	AGACCCGTGA GCACATTGCTG	CTTGCCCGTC	50
AGGTCGGTGT CCAGAAAGATT	GTCGTCTTCG TCAACAAAGGT	CGATGCCATT	100
GACGACCCCTG AGATGCTTGA	GCTCGTCGAG ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC GGCTTCGAGG	GTGACGAGAC CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC CCTCCAGAAC	CAGCGCCCCG AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC TTGCCGCCGT	TGACGAGTGG ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG CCCTTCCTCA	TGTCCGTTGA GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC CGTCGTCTCT	GGCCGTGTCG AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA TTGAGCTCGT	CGGCAAGGGT AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC ATTGAGACCT	TCAAGAAAGTC TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACTC TGGTCTCCTC	ATCCGAGGTG TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG TCGTCTGCGC	CCCCGGCACT GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC CTCTACGTCC	TCACCAAGGA GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA GCACTACCGA	CCCCAGCTCT ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC TGACCTTCCC	CGAGGGTACC GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCG GGTGACAACA	CCGAGATGGT CATCACCATG	GGCCACCCCA	800
ACGCCATTGA GGTCGGTCA			819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
- (B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC CAAATGTAAG	ACGCCGGAG GGAGTGTGA	AGGTTTTATG	50
CTTTTTAGGC CCTTTGTTTC	TGAGAGCATG ATGATACTAA	TACTCGGAAA	100
CGTATCTATT AGGCCTAAA	CACGTGAGCA TTTGCTCCTT	GCCCAGACAGG	150
TCGGTGTCCA AAAGATCGTC	ACAAAGTCGA CGCCCTTGAG	200	
GACAAGGAGA TGTTGGAGCT	TGTCGAGTTA GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA TTTGAGGGTG	AAGAGACACC CATCATCTT	GGTTCTGCC	300
TTTGCGCCAT GGAAGGCCGT	GAGCCTGAGT TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG AGGCTGTTGA	TACTTGGATC CCAACACCAC	AACGTGATAC	400
CGAAAAACCT TTCTTGATGT	CCGTTGAGGA AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT TGCCTCCGGT	CGTGTGAGC GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACCTCCGG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTCTT	TTTTTCCTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTT	TCAACTCGCC	TGATTACACGA	AATTAACTAA	900
CCCCTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

2) INFORMATION FOR SEQ ID NO: 2200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCCT	GCTGGTCGCC	50
CTGAACAAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCCGCTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCGTGG	TGACCGGTGCG	CGCCGAGCGC	350
GGGACCCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCGAT	400
CCAGAACGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTGG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

2) INFORMATION FOR SEQ ID NO: 2201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio mimicus*
 (B) STRAIN: ATCC 33653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTGCGCAAGT	AGGTATTCC	TACATCATCG	TATTCA	TGAA CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAGCACT	AGGCAGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAACTAG	CAGAACGACT	AGATTCA	ATTC	CAGAGCGTGC	300
AGTAGACATG	GCATTCC	TGCCAATCGA	AGACGTATT	TCAATCCAAG	350
GTCTGGTAC	AGTAGTA	GGCGTATCG	AGCGCGGCAT	CCTGAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCACTGCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCCACACA	CTAAGTTCGA	600
ATCAGAAAGTA	TACGTACTGT	CAAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAACA	700
GGCAGCATCG	AGCTTCCAGA	AGGC	GTAGAA	ATGGTAATGC	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

2) INFORMATION FOR SEQ ID NO: 2202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGT	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTTAT	CGATGCAGAA	CACGC	ACTGG	ACCCGGTCTA	100
CTTGGCGTTG	ATATCGATAA	CCTGCTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCA	CTGGC	GCGCTCCGGT	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGC	CTT GCGCGT	TGATGAGCCA	300
GGCGATGCGT	AAGCTGCCG	GTAAC	CTGAA	GCAGTCCAAC	350
TTTCATCAA	CCAGATCCGT	ATGAAGATTG	GC	GTATGTT CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA TCTTATGCTA GAAATTAGG TGTTGATATA GATAACCTAA	50
TAGTTTCTCA ACCAGATACA GGAGAACAGG CTTTAGAGAT AACAGAAGCT	100
TTAGTAAGAT CAGGAGCAGT AGATGTTATA GTTGTAGACT CTGTTAGCAGC	150
TTTAGTTCCCT AGGGCAGAAA TAGAAGGAGA AATGGGAGAC TCACATGTAG	200
GTCTTCAAGC AAGACTTATG TCTCAAGCCC TAAGAAAATT AGCAGGATCT	250
ATAAAATAAAT CTAAGTGTGT AGCTATATTT ATAAACCAAT TAAGAGAAAA	300
GGTTGGTATA ATGTTTGAA ATCCAGAAC AACTCCT	337

2) INFORMATION FOR SEQ ID NO: 2204

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC GGTACTGCAG CATTGTTGA TGCTGAGCAT GCACTAGATC	50
CAAATATGC AAAGCTTTA GGTGTTGATG TTGATAATCT GATCGTGTCA	100
CAGCCGGATA CGGGTGAGCA AGCTTTAGAG ATTGCTGATA TGTTGGTACG	150
TTCTGGAGGA GTTGATATTG TAGTAATTGA CTCTGTTGCT GCACTTACGC	200
CAAAGGCAGA GATTGAGGGT GACATGGGCG ACTCGCACAT GGGCTTACAA	250
GCAAGATTAA TGTCACAAGC ACTAAGAAAA CTAACGGCAA ATATCAAGCG	300
CTCAAATACT CTAGTGTAT TCATTAACCA AATTCTGTATG AAGATCGGGG	350
TTATGTTGG TAACCCTGAA ACTACAAC	379

2) INFORMATION FOR SEQ ID NO: 2205

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
- (B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA GTATATGCAA GGGCTCTTGG AGTGGATATA GACAACCTAG-	50
TCATATCTCA GCCAGATACA GGAGAACAGG CCCTAGATAT AGCAGAGTCC-	100
CTTATAAGAT CAGGAGCTGT AGATATACTA GTAATAGACT CAGTAGCTGC-	150
CCTAGTACCT AAGGCAGAAA TAGAAGGTGA CATGGGAGAT TCTCACGTAG-	200
GTCTACAGGC TAGACTTATG TCACAGGCAC TTAGAAAATT GACTGGATCT-	250
ATAAAGAAGT CAAACTGTGT TGTTATATT, ATCAACCAGT TGAGAGAAAA-	300
AGTAGGGGTT ATGTTCGGTA ATCCAGAGAC AACAAACA	337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
- (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT GGATATGCAA AAAACCTTGG AGTAGATGTA GAAAATTAA-	50
TTATTTCTCA ACCTGATACA GGTGAGCAAG CCTTAGAAAT AACTGAAGCT-	100
CTTGTAAGAT CTAACGCTGT TGATTTAATT ATTATAGACT CAGTTGCCGC-	150
ACTTGTACCA AAAGCAGAAA TCGATGGTGA CATGGGAGCT GCACAAATAG-	200
GTCTTCAAGC AAGACTTATG TCTCAAGCTC TTAGAAAATT AACTGGGGCA-	250
ATCAAACAAGT CAAAATGTAC CGTTGTATTT ATTAACCAAC TTAGAGAAAA-	300
AGTTGGTATC ATGTTGGTA ACCCAGAAAC TACAACA	337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC AAGTTATTGC AGCAGCACAA CGTAGCGGAA AAACCTGTGC	50
ATTATCGAC GCTAACATG CGCTAGATCC AATCTATGCG AAAAAACTGG	100
GTGTTGATAT CGATAACCTT CTATGTTCTC AACCTGATAC TGGTGAGCAA	150
GCATTAGAGA TTTGTGATGC ACTGACGCGT TCAGGCGCTG TTGATGTCAT	200
TATCGTTGAC TCCGTGGCCG CATTAAACACC AAAAGCTGAA ATTGAAGGTG	250
AAATCGGTGA CTCACACATG GGCTTAGCGG CTCGTATGAT GAGCCAAGCG	300
ATGCGTAAAT TAGCGGGTAA CTTAAAGAAC TCGAATACAC TTTTAATCTT	350
CATTAACCAA ATCCGTATGA AGATTGGCGT TATGTTGGT AACCCAGAAA	400
CCACTACA	408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG ATTGCCGCTG CGCAGCGTGA AGGTAAAACC TGTGCGTTA	50
TCGATCCGA ACACCGCGTT GACCCTGTTT ACGCACGCAA GCTGGCGTC	100
GATATCGATA ACCTGCTTG TTCTCAGCCG GATACCGGCG AGCAGGCGCT	150
GGAAATCTGT GACGCGCTGG CGCGTTCAGG CGCGGTGGAC GTCATTGTGG	200
TCGACTCCGT AGCGGGCGTA ACGCCGAAAG CGAAATCGA AGGGAAATT	250
GGCGACTCTC ACATGGGCCT CGCGGCGCGT ATGATGAGCC AGGCGATGCG	300
TAAGCTGGCG GGGAACCTAA AACAGTCCAA CACGCTGTTG ATTTTCATCA	350
ACCAAGATCCG TATGAAGATT GGCGTGATGT TCGGTAACCC GGAAACCACC	400
ACC	403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCAG	150
GCAGGCGCTG	GAAATCTGTG	ACCGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	CGGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTCATCAA	CCAGATCCGT	ATGAAGATTG	GC GTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GT TTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATT TATCTCA	ACCTGATCAT	GGGGAAACAAG	GT TTAGAAAT	TGCCGAAGCA-	100
TTTGTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCCAGGCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTCAAAAT	CAAATACAAC	AGCAGTATT	ATCAACCAAA	TCCGTGAAA-	300
AGTTGGTGTG	ATGTTCGGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTAA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGGCACTG	GAAATTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAGC	TGAAATTGAA	250
GGTGAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCAC	TTGCAAACCA	TCGCGGAAAT	GCAAAACTG	GGCGGCACCT	50
GCGCGTTAT	CGACGCCGAG	CACGCAGTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTCGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

2) INFORMATION FOR SEQ ID NO: 2213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG ACATGATTTC CGAAGAAGAC GCTGAAGGCA CG

42

2) INFORMATION FOR SEQ ID NO: 2214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCCT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAAACGGAG AATAA	125

2) INFORMATION FOR SEQ ID NO: 2215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGGCACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACCGAGTAA	140

2) INFORMATION FOR SEQ ID NO: 2216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

2) INFORMATION FOR SEQ ID NO: 2217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

2) INFORMATION FOR SEQ ID NO: 2218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGAACGGC ACTGCCTAA	119

2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG CGTTCTCTGA CCAAAGGTCTG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCTAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AGTAA	115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG CGTTCTCTGA CCAAAGGTCTG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCGAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AATAA	115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTAA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCCAAGGCCG GGCGAACTAC TCCATGGTCT	50
TCGACTCTTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonaee*
- (B) STRAIN: Mgord-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAACTA CTCCATGGTG	50
TTCGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTCGAAGG AGATCATCGC	100
GAAGGCGACGG GGCAGATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG CGGTCCAAGA CTCAAGGCCG GGCGAACTAC TCGATGGTGT	50
TCGATTCTTA CGCCGAAGTG CCGGCTCAGG TGTCGAAGGA GATCATCGCG	100
AAGGCGACTG GCGAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG CGGTCGAAGA CCCAGGGCCG GGCGAACTAC TCCATGGTGT	50
TCGACTCTTA CGCCGAAGTG CCAGCGCAGG TGCGAAGGA GATTATCGCG	100
AAGGCAACGG GCGAGTAA	118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG CGTTCTGCAA CCCAAGGCCG CGCTACTTAC TCTATGGAGT	50
TCAAGAAATA TTCTGAAGCT CCTGCCACA TAGCTGCTGC TGTAAGTCAA	100
GCCCCGTAAAG GCTAA	115

2) INFORMATION FOR SEQ ID NO: 2227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACCA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACCA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAAATCAA TTGCTGATGA TATCATCAA	100
AAAAATAAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

CGTTCAATGC	GTGTTCTAGA	CGGTGCAGTT	ATGGTTTACT	GTGCTGTGGG	50
TGGTGTTCAG	CCTCAGTCTG	AAACCGTTG	GAGACAGGCT	CAGAAAGTACA	100
AGGTTCCCTCG	TATTGCTTTC	GTAAATAAGA	TGGACCGTAC	TGGTGCTAAT	150
TTCCTACGTG	TTGTAGAGCA	GATTAAGACC	CGTCTAAAGG	GTAAACCCTGT	200
TCCTCTAATG	TTACCTATCG	GTAAAGAGGA	CAGCTTGTGTT	GGTGTAGTTG	250
ACCTAACCAA	GCGTAAGGCT	ATCGACTGGG	ATGAGGCATC	TCAGGGTATG	300
AAGTTTGAGT	ACGTTGACAT	TCCAGCAGAT	ATGGTTGAGG	AAGTTGAAGA	350
GTGGCGTGCA	AAGCTTGTAG	AAGCAGCTGC	AGAAGCTAAC	GACGAGCTGA	400
TGGATAAATT	CTTCGGTGGT	GAAGAGCTGA	CCGAGGAAGA	GATCAAGGCT	450
GCTCTACGTG	AGCGTACTCT	TCGCAACGAA	ATTATTCTA	TGTGCTGC GG	500
TTCAGCATT	AAGAACAAAGG	GTGTTCAGGC	AATGCTTGAC	GCTGTTGTTG	550
AGTATCTTCC	ATCTCCAGCA	GATGTTCCCTG	CTGTTGAGGG	TAAGACCCTA	600
ACCGGTGAAG	CTGATACTCG	TAAGGCTGAC	GATAAAGAGC	CATTCTCTGC	650
TTTAGCATT	AAGCTAGCAA	ATGACCCATT	CGTAGGTAAC	TTAACATTCT	700
TACGTTGCTA	CTCAGGCTTT	ATTAAGTCTG	GTGACACTGT	AATGAACTCA	750
GATAAAGCAGA	AGCGTGAGCG	TTTCGGCCGT	CTAGTTCAGA	TGCACGCTAA	800
TGCTCGTAAT	GAGGTTAGCG	AGGTTATGC	AGGTGACATC	GTTGCTGCTA	850
TTGGTCTGAA	GGAAACCGTT	ACCGGTGATA	CCTTATGTGA	CCCAGAGCAT	900
CCAATCATT	TTGAGTCAAT	CGACTTTGCA	GAGCCAGTTA	TCTCTGTAGC	950
AGTTGAGCCT	AAGACCAAGG	ACGATCAGGA	GAAGATGGCT	CTTGCTTTAC	1000
AGCGTTTAGC	AAAAGAAGAT	CCTTCATTCC	GGGTTCGTAC	AGACGAAGAG	1050
TCTGGCCAGA	CCATTATTT	TGGTATGGGT	GAGCTTCACC	TAGACATCAT	1100
TGTTGACCGT	CTACGCCGTG	AGTTCAAGGT	TGAGTGTAA	CAGGGTAAGC	1150
CACAGGTTGC	ATACCCTGAG	ACCATTAAGA	GCAAGGTTGA	ACAGCAAGGT	1200
AAGTTTGCTC	GTCAGTCTGG	TGGTCGTGGT	CAGTACGGTG	ACTGCTGGTT	1250
ACGTATGGAA	CCTCTTGAGC	CAGGTAAGGG	CTACGAATT	GTGAATGAGA	1300
TTGTTGGTGG	TGTAATTCT	AAGGAATATA	TCCCCTGCAAT	TGATAAGGGC	1350
TGTCAGGAGC	AGATCGCTAA	CGGTGTTCTA	GCTGGTTTCC	CAGTTGTTGA	1400
CATCAAGATC	ACTGTATT	ATGGTTCTTA	CCACGAAGTT	GAECTTTCAAG	1450
AAATGGCATT	CAAGATTGCT	GCTTCTATGG	CATTCAAAGA	GGGCTTCAAG	1500
AAGGCAAATC	CTGTTCTTCT	AGAGCCTT	ATGAAGGTAG	AAGTTGATAC	1550
TCCTGAAGAC	TACATGGGTG	ACGTTATTGG	TGACTTAAAC	CGTCGTCGTG	1600
CTATCGTTGA	AGGCATGGAA	GATGGTCCTA			1630

2) INFORMATION FOR SEQ ID NO: 2230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTCATTG	CGTGTGCTAG	ACGGTCAGT	TACTGTCTTG	50
GACTCACAAAT	CAGGTGTTGA	ACCACAAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTGTAaaa	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCCTT	CTCCAACCGA	CGTTCCCCCA	ATTAAGGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTCAT	CACTTGCTTT	TAAAGTTATG	TCAGACCCCTT	ATGTTGGCCG	700
CTTAACCTTC	TTCCGTGTTT	ATTCAAGGTGT	GTTGGATACA	GGTTCTTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGCTGCT	GTAAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACCTCAA	1100
TTAGACGTTC	TTATTGACCG	TATGAAGACT	GAATTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTAC	TCCAAACGAA	GAAGGAGCAG	GATTGAATT	1300
TAAAAAACTCC	ATTGTTGGTG	GGGTTGTCCTC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAGGC	AGAACTGTTT	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTC	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

2) INFORMATION FOR SEQ ID NO: 2231

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1652 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Veillonella parvula*
 - (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTACTTGACG	GTTCTGTTGC	GGTGTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAACCTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTGG	AAGGCAGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCCCTGGTAC	TGAAGAAGAA	ACAACTCGTC	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTACT	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACCGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	ACACAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTCGTACTG	1050
ATGAAGAAC	AGGTCAAAC	ATTATCTCTG	GTATGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTTAA	ATTCGTACGT	CAATCTGGTG	GTGCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTGA	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCTCG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCC	1400
ATGTTGATG	TTAAAGTTAT	CGTATTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCCT	GCATTGCTTG	AACCATAATAT	GGCTGTAGAA	1550
GTAGACGTTTC	CTGAAGAATA	CATGGCGAC	GTTATCGGTG	ACTTGAACTC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

2) INFORMATION FOR SEQ ID NO: 2232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTCGTACTG	50
CAGTTGGTGG	TGTTCAGCCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCGTT	AACAAAATGG	ACCGTATGGG	150
TGCGAACCTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCAG	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTCACCGGT	250
ATTATCGATC	TGGTAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGCGTGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACCTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCTGTTGGT	700
AACCTGACGT	TCTTCCCGT	GTACTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTCTGAAC	TCAGTGAAT	CGAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100	
ATTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAACGA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCATCAT	TGCCACCGGG	TGGTGTGTTGG	1300
TATGAATTCTG	TCAACGAAAT	CGTTGGTGGT	TCTATTCTA	AAGAATTCTAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACAA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCCTGACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

2) INFORMATION FOR SEQ ID NO: 2233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGCCGGTGT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACCTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTCTG	ACTACGTCGA	TATTCTGCA	GAGCTGGCTG	ATTCCGCCGC	350
CGAGTGGCGC	AAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACAA	AGGGCGTACA	GGCCATGCTG	GACGCCGTCA	550
TCGAATAACCT	GCCATCGCCA	CTGGACATCG	ACGATGTGG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTCGTCGGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACCACGGCG	AAACCCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCCGCGTGA	GACCGATGAA	1050
GAATCAGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTCTGG	CGTGGAAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAAACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCCAGG	CAAGGGCTTC	GAGTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCCCTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCCTGC	GCGGCACCCCT	GAACACCCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGACGTC	AAGGTACACGC	TGTTCTTCGG	TTCGTACACAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCCAG		1636

2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTCAT	GATCGGTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTCA	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCTGTAG	GCTTTGCGCTT	CTTCCAGCGG	GTACATGTCG	400
ATCACAAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACCC	TACGTTCGCT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGGCCAGAC	650
GGCCCAGAGC	CAGGCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGGATGAT	750
CGCGCTTTT	TCGTACACAC	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATA CGGCCA	AAAC GCTCGC	GCTT CTCTTT	900
AACGGAGTTC	AGCACCGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAACGA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAAG	GATGATTTCG	TTGTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCCTT	GCGCTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTGATGGCT	TTCATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
				GGAACG	1656

2) INFORMATION FOR SEQ ID NO: 2235

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Abiotrophia adiacens*
 - (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAAC	TCAATTAAATA	GGAGGAATCA	150
TTTAA					155

2) INFORMATION FOR SEQ ID NO: 2236

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter baumannii*
 - (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAACAAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

2) INFORMATION FOR SEQ ID NO: 2237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACC GG GTGAGTGG GGGCGGGCA ATCGGCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCCATGGG TGTTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTTACCG CGAGTCCAGG AGGACGAAAA	150

2) INFORMATION FOR SEQ ID NO: 2238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
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2) INFORMATION FOR SEQ ID NO: 2239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCACATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCCTAG	GATCATGTAA	200
CTGGCACAAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCCACGAA	300
GTCCAGGAGG	ACACACA				317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2242

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Listeria monocytogenes*
 - (B) STRAIN: ATCC 15313

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAACT ATTACTTAGT TTAAATTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTTAAA	126

2) INFORMATION FOR SEQ ID NO: 2243

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium avium*
 - (B) STRAIN: ATCC 25291

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGGGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

2) INFORMATION FOR SEQ ID NO: 2244

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

1153

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonaee*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC	50
AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC	100
AAA	103

2) INFORMATION FOR SEQ ID NO: 2245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

GCCGAGCGTT GCGCGTAAGC TAGCTCGTT ACCACGGCGG CAAAACTAGA	50
AAAACATCAA CACTGCTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA	100
A	101

2) INFORMATION FOR SEQ ID NO: 2246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAAACCAA AAAGATCAAT	50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A	91

2) INFORMATION FOR SEQ ID NO: 2247

1154

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria polysaccharea*
 - (B) STRAIN: ATCC 43768

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTC AGACGGCATT	50
GTTCCTTAAT CGATCTTAA TGTAAGGAA TTAGCTC	87

2) INFORMATION FOR SEQ ID NO: 2248

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus epidermidis*
 - (B) STRAIN: ATCC 14990

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTA TGATTTGATT TTTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTAAATA	218

2) INFORMATION FOR SEQ ID NO: 2249

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus haemolyticus*
 - (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACCTTGT TTTAGCTAGA ATTTCTAGGT AAAATACAGC GTAAGCTTAT	50
TAATTAAGCT AACATCTTA TGAATTGATT TTTTACTGAA AATGCATTAT	100
AAATGAATTA TGAATTCTAA CAATCATTAT GTCTCATGAT GGTGAGAAC	150
TATCATGAGA GATAATATTG AAATAACTTT TACTAGAATA GGAGAGATT	200
AATA	204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS: ,

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG GTGTCGTATA CCGCGGAGTC GCCGACGG	38
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2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS: ,

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT CTCGCTGCGT TACATGCTGG TGGCTCCG	38
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2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS: ,

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG TGTCTCTC	18
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2) INFORMATION FOR SEQ ID NO: 2253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

2) INFORMATION FOR SEQ ID NO: 2254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG AAAAATTTGA CCGTTAAAAA CCACACGTTA ACATTGGTAC	50
AATCGGCCAC GTTGACCACG GTAAAACAAC ATTAACTGCT GCTATCACAA	100
CTGTTTAGC TAAGAAAGGT TTTCGCGCAAG CTCAAGATT A CGGTTCAATC	150
GATAAAAGCTC CAGAAGAACG CGAACGTGGT ATCACAATCA ACACCTTCTCA	200
CGTTGAGTAC GAAACAGACA CTCGTCACTA TGCTCACGTT GACTGCCAG	250
GACACGCGGA CTACGTTAAA AAC	273

1157

2) INFORMATION FOR SEQ ID NO: 2256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG CCAAGTTGA ACGTAATAAA CCACACGTAA ACGTGGGTAC	50
AATCGGTAC GTTGACCATG GTAAAACAAC TTAACTGCT GCGATTGCAA	100
CAATTGTGC AAAAACTTAC GGCGGTGAAG CGAAAGATTAA CTCACAAATC	150
GACTCAGCAC CTGAAGAAAA AGCACGTGGT ATTACAATTAA ATACATCACA	200
CGTAGAATAAC GATTCTCCAA CTCGTCACTA CGCACACGTT GACTGCCAG	250
GCCACGCCGA CTACGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG CCAAGTTGA GCGCACCAAG CCGCACGTCA ACATCGGCAC	50
GATTGGTCAC GTTGACCAAGC GCAAGACGAC GCTGACGGCA GCTATCACCA	100
AGGTGCTGCA TGACAAAGTAC CCCGAACGTGA ACGAGTTCAC CCCCTTCGAT	150
CAGGTGACAA ACGCTCCCAGA GGAGCGCGAT CGTGGCATCA CGATCAACGT	200
CTCTCACGTT GAGTACCAGA CCGAGGGCGCG TCACTACGCG CACGTTGACG	250
CTCCCGGCCA CGCCGACTAC GTCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG AAAAATTGTA TCGTTCCCTA CCGCACGTCA ACGTTGGCAC	50
TATCGGTAC GTTGACCATG GTAAAACAC TCTGACTGCT GCTCTGACTC	100
GCGTTGCTC CGAAGTATTG GGTTCCGCAA TCGTTGATTG CGATAAAATC	150
GACAGCGCAC CAGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCGCGCA	200
CGTTGAATAAC AACTCGCTGA TCCGTCACTA CGCTCACGTT GACTGCCAG	250
GTCACGCTGA CTATGTGAAG AAC	273

2) INFORMATION FOR SEQ ID NO: 2259

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG CTAAGTCGA GCGTACCAAG CCGCACGTCA ACATCGGCAC	50
CATCGGTAC GTTGACCAAG GTAAGACAC CACCACCGCT GCTATCACCA	100
AGGTTTGCGC AGACGTTAC CCAGAGCTGA ACGAAGCTTT CGCTTTCGAT	150
GCCATCGATA AGGCACCGGA AGAGAAAGAG CGTGGTATTA CCATCAACAT	200
CTCCCACGTG GAGTACCAAGA CCGAGAAGCG CCACTACGCA CACGTTGACG	250
CTCCAGGTCA CGCTGACTAC ATCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2260

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG AAAAATTTGA ACGTACAAAAA CCGCACGTCA ACGTTGGTAC	50
TATCGGCCAC GTTGACCATG GTAAAACCTAC CCTGACTGCT GCAATCACTA	100
CCGTTCTGGC TAAAACCTAC GGTGGTCTG CTCGTGCATT CGACCAGATC	150
GATAACGCAC CAGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTCTCA	200
CGTTGAATAT GACACCCCGA CTCGCCACTA CGCACACGTA GACTGCCAG	250
GTCACGCCGA CTATGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2261

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG AAAAATTTGA ACGTACAAAAA CCGCACGTCA ACGTTGGTAC	50
TATCGGCCAC GTTGACCATG GTAAAACCTAC CCTGACTGCT GCCATCACTA	100
CCGTTCTGGC TAAAACCTAC GGTGGTCCG CTCGCGCATT CGACCAGATC	150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTCTCA	200
CGTTGAATAT GACACCCCGA CTCGCCACTA CGCGCACGTA GACTGCCGG	250
GCCACGCCGA CTATGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2262

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAG AAAAATTTGA CCGCTCTAAA CCCCATGTTA ACATTGGTAC	50
TATTGGACAC GTTGACCATG GTAAAACAAC TTTAACTGCT GCAATTACAA	100
1160	

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACGTACA	GCCGTCACTA	TGCACACGTT	GACTGCCAG	250
GACATGCCGA	TTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCACG	GCAAGACCAAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCC	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAAGA	CCGACAAAGCG	GCAC TACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonaie*
- (B) STRAIN: Mg or-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCACG	GCAAGACCAAC	TCTGACCGCG	GCTATCACCA	100
AGGTCTTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAAGA	CCGAGAAAGCG	TCAC TACGCG	CACGTCGACG	250
CCCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG CGAACGTTCCA GCGGACCAAG CCCCACGTCA ACATCGGGAC	50
CATCGGTACG GTTGACCCACG GCAAGACCAAC CCTGACCGCG GCTATCACCA	100
AGGTCTGCA TGACAAGTTC CCGGACCTGA ACGAGTCGAA GGCGTTCGAC	150
CAGATCGACA ACGCTCCTGA GGAGCGCCAG CGCGGTATCA CGATCAACAT	200
CGCGCACGTG GAGTACCAAGA CCGAGAAGCG GCACTATGCA CACGTCGACG	250
CGCCGGGCCA CGCCGACTAC ATCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG CGAACGTTCGA GCGGACGAAG CCCCACGTCA ACATCGGGAC	50
CATCGGTACG GTTGACCCACG GCAAGACCAAC GCTGACCGCG GCTATCACCA	100
AGGTTCTGCA CGACAAGTAC CCGGACCTCA ACGAGTCGCG TGCCTTCGAC	150
CAGATCGACA ACGCTCCCGA AGAGCGTCAG CGCGGTATCA CCATCAACAT	200
CTCCCACGTG GAGTACCAAGA CCGAGAAGCG GCACTACGCC CACGTCGACG	250
CTCCTGGTCA CGCTGACTAC ATCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG AAAAATTGCA ACGTAGCAAA CCGCACGTAA ACGTTGGCAC	50
CATCGGTAC GTTGACCATG GTAAAACCAC TCTGACTGCT GCTTTGACTA	100
CTATTTGGC TAAAAAATTC GGCGGTGCTG CAAAAGCTTA CGACCAAATC	150
GACAACGCAC CCGAAGAAAA AGCACGCGGT ATTACCATTA ACACCTCGCA	200
CGTACAATAAC GAAACCAGAA CCCGCCACTA CGCACACGTA GACTGCCGG	250
GTCAAGCCGA CTACGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAAG AAAAATTGCA TCGCTCAAAA GAACATGCCA ATATTGGTAC	50
TATCGGTAC GTTGACCATG GTAAAACAAAC TTTAACAGCT GCTATCGCAA	100
CTGTATTAGC TAAAAATGGT GACACTGTTG CACAATCATA CGATATGATT	150
GACAACGCTC CAGAAGAAAA AGAACGTGGT ATTACAATCA ATACTGCACA	200
TATCGAATAAC CAAACTGACA AACGTCACTA TGCTCACGTT GACTGCCAG	250
GACACGCTGA CTATGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTGATCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTAC	GTTGACCATG	GTAAAACACTAC	TTTAACAGCT	100
CTGTATTAGC	TAAAATGGT	GACACTGTAG	CACAATCATA	150
GACAAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAAATCA	200
CATCGAGTAT	CAAACGTGACA	AACGTCACTA	TGCTCACGTT	250
GACACGCTGA	CTATGTTAAA	AAC		273

2) INFORMATION FOR SEQ ID NO: 2270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GAETCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGGTGTG	TAGAGCGCGG	400
TATCGTAAA	GTTGGTGAAG	AAAGTGGAAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCAC	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACGTCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

2) INFORMATION FOR SEQ ID NO: 2271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TGGCGTGCC	TCACCTCGTC	GTGTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCCTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCTGA	TGCCCATCGA	AGACGTGTT	TCCATCTCCG	350
GCCCGGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGAACGC	550
GGCCAGGTTC	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCAGGCCGC	CATAACCCGT	650
TCTTCACCGG	CTATCGTCCT	CAGTTCTACT	TCCGTACAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCAGTTGAA	ATGGTTATGC	CCGGCGATAAA	750
CGCTACCTTT	AATGTCGAGC	TCATTACCCC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCCGCGAGC	50
ACATCCTGCT	GTCGCGTCAG	GTCGGCTTC	CGGGCGCTGGT	GGTGTTCCTG	100
AACAAGGTCTG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCCTC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCCTGATG	CCGGTGGAAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCTG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTCGATCAC	600
CCCGCACACC	AAGTTCTGAA	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGCCGTCA	CACGCCGTTC	TTCACGAAC	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCCTC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCGA		786

2) INFORMATION FOR SEQ ID NO: 2273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCAATTGAA	100
ATTCCTCAAT	GGCCTTGGTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAAATGG	CTGCCGCTTA	CGCTGCCCTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAG	TCTGGAACTG	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAACATT	TGTTGGCTAT	ACTCCACAAT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCAACA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTGGTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACAAC	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAAATGG	CTGCTGCCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTCTACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA AATTGAAAAG TATATCAAGA ACACGGCTA CGTAGCCCCA	500
GATGAAATGT TTGTAGGGTA TACTCGAAA TATGCAATGG CTGTTGGAC	550
A	551

2) INFORMATION FOR SEQ ID NO: 2275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear.

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG CTGGATTACT ATCCAATACG CTATCCAAGA ATCCCGTAAC	50
GTACCAGCCG TCAAATCGCT GGAAGCAGTC GGATTAGATA ATTCAATTGAA	100
GTTCTCTCAAT GGCCTTGGTA TTAATTACCC TGAAATGCAT TATTCTAATG	150
CGATTTCAAG TAATACAAGC GAATCTGGTA ACCAATACGG AGCAAGTAGC	200
GAAAAAAATGG CTGCCGCTTA CGCTGCCCTT GCTAATGGCG GTACATATTA	250
CAAACCGCAA TACGTCAACC GAGTTGTCTT TAGCGACGGT ACAGAAAAAG	300
TCTTTTCAAA TGGCGGATCA AAAGCCATGA AAGAAACGAC AGCCTACATG	350
ATGACAGACA TGATGAAGAC CGTTCTCAA TCTGGAACTG GTACCAATGC	400
TGCAATTCCA GGAGTCTATC AAGCAGGTAA AACCGGCACT TCCAACTATG	450
CAGATGATGA ACTAGAGAAG TTGACAAAAC CTTATTACAG TTCTAGCATT	500
GTCACACCAAG ACGAGCTGTT TGTTGGCTAC ACTCCACAGT ACTCTATGGC	550
TGTTTGGACA	560

2) INFORMATION FOR SEQ ID NO: 2276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGA AATATCACCA TCCAATATGC GCTCCAACAA TCACGGAACG	50
TTACAGCCGT AGAAACCTTG AACAAAGTCG GTTTGGATAG AGCCAAGACC	100
TTCCTGAATG GAATCGGTAT TGACTATCCA GATATGCACG ATGCCAACGC	150
GATTCAAGT AATACGACTG AGTCAAACAA AAAGTACGGA GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATA	450
AGATGATGAA	ATTGAAAAT	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

2) INFORMATION FOR SEQ ID NO: 2277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAAA	TCTGCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAAC TGATG	350
GCCGAT					356

2) INFORMATION FOR SEQ ID NO: 2278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAAT	CAGCCCGTGT	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT CGTCGTATG	GCCCAGCCGT TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC AGGGAACTT	CGGTTCAATC GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT ACGGAAATCC	GTCTGGCGAA AATTGCTCAC	GAACTGAA	347

2) INFORMATION FOR SEQ ID NO: 2279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA TCTGGATTAT	GCGATGTCGG TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC GAGATGGCCT	GAAGCCGTA CACCGTCGCG	TACTTACGC	100
CATGAACGTA CTAGGCAATG	ACTGGAACAA AGCCTATAAA	AAATCTGCC	150
GTGTCGTTGG TGACGTAATC	GGTAAATACC ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA CGATCGTCCG	CATGGCGCAG CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC GGTCAGGGTA	ACTTCGGTTC TATCGACGGC	GACTCTGC	300
CGGCAATGCG TTATACGGAA	ATCCGTCTGG CGAAAATTGC	CCATGAACTG	350
ATGGCCGATC TC			362

2) INFORMATION FOR SEQ ID NO: 2280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG GATTATGCGA	TGTCGGTCAT TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA TGGCCTGAAG	CCGGTACACC GTCGCGTACT	TTACGCCATG	100
AACGTACTAG GCAATGACTG	GAACAAAGCC TATAAAAAAT	CTGCCGTGT	150
CGTTGGTGAC GTAATCGGT	AATACCATCC CCATGGTGAC	TCGGCGGTT	200
ATGACACGAT CGTCCGTATG	GCGCAGGCCAT TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC AGGGTAACCTT	CGGTTCCATC GACGGCGACT	CTGCGCGGC	300
AATGCGTTAT ACGGAAATCC	GTCTGGCGAA AATTGCCAT	GAACTGATGG	350
CCGATCTC			358

2) INFORMATION FOR SEQ ID NO: 2281

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCCAGCTG GGCGGCGGTA TCGATGGGGG

30

2) INFORMATION FOR SEQ ID NO: 2282

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

2) INFORMATION FOR SEQ ID NO: 2283

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAAGAG GC

22

2) INFORMATION FOR SEQ ID NO: 2284

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

1170

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTT	TATAAATAAG	TTATTCGTT	ATTTTGTTT	50
TGTGCTAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTC	AGTTTTAAAT	GCCATTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTAA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCG	GCGCAGGCCT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCCCTTATG	TACCACTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTGAT	CAATGTGAAG	GTTCTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTTCTAGT	GTCGGCATTA	CAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAAGCG	GATTGAGCCG	GTGCGATTTC	1000
TTTTTGACAA	ATAAAAATGA	ATTATTCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTCAG	GAGTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAAATACGG	TGATTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTGAAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACCGCGT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

2) INFORMATION FOR SEQ ID NO: 2290

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

2) INFORMATION FOR SEQ ID NO: 2291

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

2) INFORMATION FOR SEQ ID NO: 2292

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

2) INFORMATION FOR SEQ ID NO: 2293

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1032 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCAC	GGAATGGGAA	AACGACAATT	GCTATTCAAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACCC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTGTA	GGCTGCGATA	TTCAAAGCTC	AGCAATTGTT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATT	ATAAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATT	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCCTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCCT	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAC TGATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTCGG

18

2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTGCA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCC GGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTTC	AAAGCTCCGC	AGCTTGATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTCGTC	CTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTGATTGT	CGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
GCAGAGGGCT	TGCTCGTGT	GATCTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GC GGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17